U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

SEARCH REQUEST FORM

Requestor's Name:		Serial Number:		_
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Search Topic: Please write a detailed statement of sear terms that may have a special meaning. please attach a copy of the sequence. You	Give examples or releven	it citations, authors, keyv	vords, etc., if known. For sequences,	
Date completed: 0 5-07-01	STAFF US	E ONLY	¥7 1	
Searcher: Perent C		STIC	Vendors	
Terminal time: 201		CM-1	STN	
Elapsed time:		Pre-S	Dialog	
CPU time: 2-8		of Search	APS	
Total time: 2.8 Number of Searches:		N.A. Sequence A.A. Sequence	Geninfo SDC	
Number of Databases:	.	_	DARC/Questel	
1			Other CGN	

PTO-1590 (9-90)

Tue May

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- protein search, using sw model protein MO

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3, 2002, 16:24:41; Search time 117.39 Seconds (without alignments) 161.536 Million cell updates/sec

US-09-534-229C-1 1362 Perfect score:

1 MARFAALAVCAAALLLAVAA......MLGTATGGNLDCYTQRNFAS

Scoring table:

Sequence:

522463 seqs, 74073290 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

of hits satisfying chosen parameters: Total number

522463

Minimum DB seq Maximum DB seq

length: 0 length: 2000000000 Post-processing: Minimum Match 08 Maximum Match 10

Maximum Match 100% Listing first 45 summaries

Database :

| SIDS2/gogdata/geneseg/genesegp/AA1981_DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*

Wheat chitinase pr Rye chitinase-like Rye chitinase-like A maize chitinase Tobacco endochitin Wild tomato endoch Wild tomato endoch Amino acid sequenc Wheat chitinase pr Petunia extracellu Petunia hybrida ex Description SUMMARIES AAB18903 AAR76714 AAR76712 AAR13274 AAW31296 AAB07512 AAB11488 AAB11487 AAW98081 AAW98082 AAR76713 22 20 20 20 11 20 21 21 22 23 DB Query Match Length 100.0 93.8 87.8 72.8 622 59.94 59.88 59.88 59.88 Score 1362 1277 1196 992 846.5 822.5 814.5 814.5 814.5 798 Result

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ALIGNMENTS

Wheat chitinase protein homologous to barley chitinase. AAB11487 standard; protein; 256 AA (first entry) Triticum aestivum. 02-MAR-2001 AAB11487; AAB11487

Wheat; chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; barley. JP2000270866-A. 03-0CT-2000

99JP-0081694. 25-MAR-1999;

(HOKK-) HOKKAIDO NOGYO SHIKENBACHO 99JP-0081694. 25-MAR-1999;

WPI; 2001-027417/04.

New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes $\,$

Claim 1; Fig 1; 11pp; Japanese.

This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression ${\sf c}$

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11-FEB-1999.
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chitinase gene in which the MRNA is extracted from a fully hardened autumn wheat P1173438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant
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100.0%; Pred. No. 8.4e-127;
Live 0; Mismatches 0;
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Best Local Similarity 100.
Matches 256; Conservative
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N-PSDB; AAX24890.
                                                                                                                   pathogenic microbes
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
(ETT46 preprotein. The mature protein, which is also claimed, is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT46 cDNA (see AAXA4890) was obtained by isolating mank from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze proteins can be used: to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological cumerials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to Ailt tumour cells. They are also used to inhibit initiation and to of diseases or spoilage caused by low temperature partogens (particularly fungi) in plants, froze foods and any cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved biological material. The signal peptide can be used cryopreserved by the pathogens or expression
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                                                                  Claim 10; Fig 22d; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 240; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secale cereale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW98082;
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RESULT
AAR76714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ΩŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ă
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                             The present sequence is winter rye (Secale cereal L. cv. Muskateer) (T4746 mature protein. It lacks the 22-amino acid signal peptide of the preprotein (see AAW98081), which is also claimed. Mature CHT46 is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT46 preprotein cDNA (see AAX24890) was obtained by isolating mRNA from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions of when only chitinases with antifreeze activity would be expressed. CHT46 and CHT9 (see AAW98079-80) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase like antifreeze proteins can be used: to increase freezing tolerance of plants and microcorganisms exposed to sub-zero contrains or conditions and microcorganisms.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAGRAIGKD 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVIT 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                materials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved biological material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLAAFF 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 20; Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A maize chitinase polypeptide designated ZmCh15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1196; DB 20
Pred. No. 2e-110;
7; Mismatches 3
                                                                                   Moffatt B, Xiong F;
                                                                                                                                                                                                       Claim 10; Fig 22c; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB18903 standard; Protein; 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.8%;
95.6%;
             98WO-CA00745
                                   97US-0903872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 95.6'
Matches 219; Conservative
                                                          (ICEB-) ICE BIOTECH INC
                                                                                  Hew C,
                                                                                                       WPI; 1999-153795/13
                                                                                                                     N-PSDB; AAX24890
                                   31-JUL-1997;
                                                                                Griffith M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB18903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208
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AAB18903
ID AAB1
XX
AC AAB1
XX
DT 08-E
XX
DE A ma.
QΩ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db
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The present sequence represents a maize chitinase polypeptide. The prescrition describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18894, AAB18895, AAB18992-05), and glucosyl hydrolase family 18 chitinases (AAB18995, AAB189907-05) and glucosyl hydrolase chitinase in plants can be modulated to enhance disease resistance in error plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence shuffling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New maize chitinase genes encoding seven chitinases of glucosyl hydrolase family 19 are useful for enhancing disease resistance in crop plants by modulating its expression in plants
Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy 18; pathogen control; disease resistance; molecular marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 PSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGM 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AFIAAANTFPGFGTTGSADDI-KRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MARFA--ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYD 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72.8%; Score 992; DB 21; Length 252; 72.8%; Pred. No. 3.6e-90; ive 23; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tobacco endochitinase PR-Q precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Page 85; 96pp; English.
                                                                                                                                                                                                                                                                                                                                         (PION-) PIONEER HI-BRED INT INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       253
                                                                                                                                                                                                                                      2000WO-US06121.
                                                                                                                                                                                                                                                                                          99US-0125915.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238 LGTATGGNLDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 72.8
Matches 187; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Yalpani N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-628269/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAA96231
                                                                                                                            WO200056908-A2.
                                                                                                                                                                                                                                   09-MAR-2000;
                                                                                                                                                                                                                                                                                       24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                              Simmons CR,
                                                                                                                                                                                 28-SEP-2000
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pcht28 (AAQ93034) and pchtI (AAQ93035), were derived from the leaves of drought-stressed L. chilense plants. The encoded childnases (AAR76712, AAR76713, respectively) may protect plants from pathogen attack during water stress. Recombinant chitinase was expressed in E. coli.
                                                                                                                                                                                                                                                                                                                                                                             Lycopersicon chilense plants, having activity against plant pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Endochitinase; wild tomato; osmotic stress; abscisic acid; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endo:chitinase gene and protein - isolated from wild tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                      2 Osmotic stress and ABA-responsive endochitinase cDNA clones,
water stress; class II chitinase; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 822.5; DB 16;
Pred. No. 2.2e-73;
2; Mismatches 60;
                                                          Location/Qualifiers
1..24
/label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 24-25; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR76713 standard; Protein; 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 60.4%;
Local Similarity 61.2%;
Les 156; Conservative 33
                                                                                                                                                                                                                                                                                 Σn
                                                                                                                                                                                     93CA-2110764
                                                                                                                                                                                                                 93CA-2110764
                                Lycopersicon chilense Dun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 ATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || |||| |:|||
ptgenldcnnqknfa 251
                                                                                                                                                                                                                                                                                 Ζ,
                                                                                                                                                                                                                                                (TABA/) TABAEIZADEH Z.
                                                                                                                                                                                                                                                                                 Tabaeizadeh
                                                                                                                                                                                                                                                                                                           WPI; 1995-269746/36.
N-PSDB; AAQ93034.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 AA;
                                                                                                                                                                                     06-DEC~1993;
                                                                                                                                                                                                                 06-DEC-1993;
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                                                                           Peptide
                                                                                                                                                                                                                                                                               Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Loca
Matches
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Lycopersicon chilense plants, having activity against plant pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sfpgfgttgddtarrkelaaffgqtshettggsl-saepftggycfvrqndq--sdryyg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRWIPTAADIAAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYIRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 alfccvfflflt----gsladgigsivtsdlfnemlknrndgrcpangfytydafiaaan 64
         tomato; osmotic stress; abscisic acid; drought; II chitinase; Lycoperison chilense.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endochitinase; wild tomato; osmotic stress; abscisic acid; drought;
                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA encoding an osmotic stress and ABA-responsive endochitinase was derived from the leaves of drought-stressed L. chilense plants. The encoded chitinase (AAR76712) shared 78% identity with that of chitinase class II isoform PR-Q of tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.2%; Score 846.5; DB 16; 63.9%; Pred. No. 9.4e-76; Live 32; Mismatches 51;
                                                                                                   1..24
/label= Sig_peptide
                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 27; 45pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR76712
ID AAR76712 standard; Protein; 253
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                                                                                                                                                                                                            93CA-2110764
                                                                                                                                                                                                                                        93CA-2110764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 63.99
Matches 159; Conservative
                                                                                                                                                                                                                                                                                                      Tabaeizadeh Z,
        ; wild class
                                                                                                                                                                                                                                                                      (TABA/) TABAEIZADEH
                                                                                                                                                                                                                                                                                                                                    WPI; 1995-269746/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 LDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 ldcyngrnf 250
                                                      Nicotiana tabacum
    Endochitinase;
water stress; c
                                                                                                                                                                                                                                        06-DEC-1993;
                                                                                                                                              CA2110764-A
                                                                                                                                                                           07-JUN-1995
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                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                     Chen R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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Length

61

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AAW31296 standard; Protein; 254 AA.
                                                                                                                                                                                                                              Example 4; Fig 1; 55pp; English.
                                                                                                                                          Vloemans AA,
                                                                                                                                 Melchers LS,
                                                               91EP-0200191.
                                                                                 90NL-0000222
                                                                                                    MOGEN INT NV.
RIJKSUNIV TE LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                  154; Conservative
                                                                                                                                                              WPI: 1991-232019/32
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                    254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTORNEA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 cyngrnfa 252
                                                                                                                                           Sela-Buurlage MB,
                                                                                                                                                                       N-PSDB; AAQ12897
        Petunia hybrida.
                                                                                                                                   Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1998
                                                               30-JAN-1991;
                                                                                  30-JAN-1990;
                                             07-AUG-1991
                           EP440304-A.
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Best Local Si
Matches 154,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW31296;
                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                 (UXLE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q
3;
                                                                                                                                                                                                                                                                    2 Osmotic stress and ABA-responsive endochitinase cDNA clones, pcht28 (AAQ93034) and pcht1 (AAQ93035), were derived from the leaves of drought-stressed L. chilense plants. The encoded chitinases (AAR76712, AAR76713, respectively) may protect plants from pathogen attack during water stress. Recombinant chitinase was expressed in E. coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRW 188
                                                                                                                                                                                                                                  Lycopersicon chilense plants, having activity against plant pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                               11 AAALILLAVAAGGAAAQGYGSVIIRSVYASMLPNRDNSLCPARGFYIYDAFIAAANTFPGF 70
                                                                                                                                                                                                                                                                                                                                                                                                            189 TPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDC
                                                                                                                                                                                                                                                                                                                                                                             7:
                                                                                                                                                                                                                         New endo:chitinase gene and protein - isolated from wild tomato
                                                                                                                                                                                                                                                                                                                                                           DB 16; Length 250;
                                                                                                                                                                                                                                                                                                                                                                               Indels
  water stress; class II chitinase; Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                         y Match 59.9%; Score 816.5; DB 16; Local Similarity 62.3%; Pred. No. 8.7e-73; hes 154; Conservative 30; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 254 AA
                                      Location/Qualifiers
1..21
/label= Sig_peptide
                                                                                                                                                                                                                                                      Claim 2; Page 26-27; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fungal resistance; phytopathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Petunia extracellular chitinase.
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                                                                                                                                                                            Yu
                                                                                                                  93CA-2110764
                                                                                                                                     93CA-2110764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                     Lycopersicon chilense Dun.
                                                                                                                                                                            Tabaeizadeh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13274 standard;
                                                                                                                                                         (TABA/) TABAEIZADEH
                                                                                                                                                                                              WPI; 1995-269746/36
                                                                                                                                                                                                                                                                                                                                 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nngknfa 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         249 YTQRNFA 255
                                                                                                                                                                                                        N-PSDB; AAQ93035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-0CT-1991
                                                                                                                    16-DEC-1993;
                                                                                                                                      06-DEC-1993;
                                                                             CA2110764-A
                                                                                                07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR13274;
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                           Chen R,
                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
                                                                                                                                                                                                                                                                                                                                                                         Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          29
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AAR13274
ID AAR1
XX
AC AAR1
XX
DT 14-0
DT 14-0
XX
XX
XX
XX
KW fung
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128 PIQLIGRSNYDLAGRALGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was deduced from a P.hybrida cDNA sequence having 80 per cent homology with tobacco clone PROB30 which encodes extracellular chitinase PR-Protein R. The gene can be inserted into an appropriate plasmid for production of transgenic plants having resistance to fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Extracellular chitinase; antifungal; transgenic plant; synergism; beta-1,3-glucanase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                 contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 254;
Roekel :
JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                               Plants with improved resistance to pathogenic fungi - othitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
    Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.8%; Score 814.5; DB 12;
62.1%; Pred. No. 1.4e-72;
iive 31; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Petunia hybrida extracellular chitinase protein
    EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31; Mismatches
  Meulenhoff F
, Woloshuk
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247 244 (first entry)

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Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant.
                                             Amino acid sequence of an extracellular chitinase.
                                                                                              Petunia hybrida
                            20-0CT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
         AAB07512;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                                         (MOGE-)
                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :
                                                                                                                                                                                                                                                                                                               This sequence represents an extracellular chitinase which is used to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase gene exhibit a synergistic antifungal effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7;
                                                                                                                                                                                                                                                                 Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 18; Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                               53;
                                                                                                                                                                                            Bol JF, Cornelissen BJC, Linthorst HJM, Melchers
Meulenhoff EJS, Sela-buurlage MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62;
                                                       59.8%; Score 814.5; DB 1
62.1%; Pred. No. 1.4e-72;
iive 31; Mismatches 62
                                     1..23
/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB07512
ID AAB07512 standard; Protein; 254 AA.
                             Location/Qualifiers
                                                                                                                                                                                                                                                                                             Example 4; Fig 1; 42pp; English.
                                                                                                                           93US-0047413
                                                                                                                                             91US-0647831
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 62.18
Matches 154; Conservative
                                                                                                                                                                                                                Woloshuk CP
                                                                                                                                                                 NV.
LEIDEN.
                                                                                                                                                                                                                                   WPI; 1997-479536/44.
                                                                                                                                                                MOGEN INT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 CYTORNFA 255
                                                                                                                                                                                                                                             N-PSDB; AAT89951
        Petunia hybrida
                                                                                                                                                                                                                                                                                                                                                                                                                   254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vloemans AA,
                                                                                                                           19-APR-1993;
                                                                                                                                             29-JAN-1991;
                                                                                    US5670706-A.
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                     Peptide
                                                         Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245
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The present sequence represents an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynucleotides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 PIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New transgenic plants expressing chitinase and glucanase have improve resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                Meulenhoff EJS, Sela-buurlage MB;
JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 WIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTAIGGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .4e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.8%; Score 814.5; 62.1%; Pred. No. 1.4
                                           /note= "signal peptide"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       LS,
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 1; 42pp; English.
                                                                                                                                                                                                                                                        91US-0647831.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.1%;
                                                                                                                                                                                     97US-0801563,
                                                                                                                                                                                                                                  93US-0047413
                                                                                                                                                                                                                                                                                                                                                                       Melchers
                                                                                                                                                                                                                                                                                                                                                                                             Woloshuk CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 154; Conservative
                                                                                                                                                                                                                                                                                                    UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                            MOGEN INT NV
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-498214/44.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   254 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248 CYTORNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAA58909
                                                                                                                                                                                                                                                                                                                                                                       BJC,
                                                                                                                                                                                                                                                                                                                                                                                               Vloemans AA,
                                                                                                                                                                                     18-FEB-1997;
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                                                                                                                                                                                                                                                           29-JAN-1991;
                                                                                         US6087560-A.
                                                                                                                                       11-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                  This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat PII73438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ë,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 evaaffggtshettggwptapdgpfswgycfkqe---qgsppsycdqsadwpcapgkqyy 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 tglWtbtardsaagrvpgygvltnvinggiecgmgqndkvadrigfykrycdifgigygn 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----YY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22 GAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKR 81
                                                                                                                                                                                                                                                                                                     New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wheat; chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; rye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.6%; Score 798; DB 22; Length 323; 59.6%; Pred. No. 8.3e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                            Wheat chitinase protein homologous to rye chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISKATSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27; Mismatches
                                               AAB11488 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR52577 standard; Protein; 266 AA.
                                                                                                                                                                                                                                                              (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
                                                                                                                                                                                                                                                                                                                                   Claim 4; Fig 2; 11pp; Japanese.
                                                                                                                                                                                                                        99JP-0081694
                                                                                                                                                                                                                                            99JP-0081694
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                 WPI; 2001-027417/04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 nldcynglsf 316
                                                                                                                                                                                                                                                                                                                                                                                                         pathogenic microbes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 NLDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                           Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                            323 AA;
245 cyngrnfa 252
                                                                                                                                                                                JP2000270866-A
                                                                                                                                                                                                                       25-MAR-1999;
                                                                                                                                                                                                                                           25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Simi
nes 149;
                                                                                         02-MAR-2001
                                                                                                                                                                                                   03-OCT-2000
                                                                    AAB11488;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                              11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR52577
ID AAR5
                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δ
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Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistan organisms. The genome of such transgenic organisms preferably contains more than one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so that the transgenic organisms have a greater degree of resistance or resistance against a wider spectrum of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 saqwpcapgkryygrgpiqlshnynygpagraigvdllanpdlvatdatvgfktaiwfwm 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               118 -----ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWM 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transgenic organisms contg. at least 2 pathogen inhibiting genes - esp. plants contg. genes with antifungal activity, show synergistic increase in disease resistance, also new DNA transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 TAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYY
                                                                                                                                                            Antifungal, pathogen; resistance; transgenic organism; synergy; crop protection; transgenic plant; chitinase; glucanase; protein synthesis inhibitor; disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jach G, Logemann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.7%; Score 772; DB 15; 56.8%; Pred. No. 2.4e-68; tive 31; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 13-14; 19pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eckes P, Gornhardt B, Schellj, Goernhardt B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 krycdilgvgygnnldcysgrpfa 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 TRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92DE-4234131.
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-136599/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 150; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 AA;
                                                                                                                                                                                                                                                                                  Hordeum vulgare L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAQ62518
                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-OCT-1992;
                                                  05-DEC-1994
                                                                                                          Chitinase G.
                                                                                                                                                                                                                                                                                                                                    DE4234131-A.
                                                                                                                                                                                                                                                                                                                                                                                               21-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chet I, 1
Mundy J,
AAR52577;
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AAR29019;
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                                                                                                                                                                                                                                                                                                   Lamb CJ,
                                                                                                                                                             Key
Region
          RESULT 14
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                    AAR29019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                 This sequence represents the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi. Plants have this enzyme to protect themselves from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease resistance on plants as
                                                                                          Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46 ggggggsvgsiinealynqmlkyskdprcpsngfyrynafitaaqsfsgfgttgdaatrk 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYIRYCGMLGTATGGNLD
                                                                                                                                                                                                                                                                      Chitinase derived from pumpkin - used to protect plants against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 756.5; DB 18;
Pred. No. 9.4e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                               (NIHA ) JAPAN ENERGY CORP.
(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
               AAW24554 standard; Protein; 292 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.5%; Sco
58.3%; Pre
tive 26;
                                                                                                                                                                                                                                                                                                   36pp; Japanese.
                                                                                                                                                                            95JP-0347367
                                                                                                                                                                                              95JP-0347367
                                                                                                                                                                                                                                                    N-PSDB; AAT79940, AAT79941
                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                           1997-380170/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                   Claim 1; Page 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ||:|
cnngrsf 292
                                                                                                                                                                                                                                                                                pathogenic fungi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTORNF 254
                                                                                                                    Cucurbita pepo.
                                                                                                                                     JP09163987-A.
                                                                                                                                                                            14-DEC-1995;
                                                                                                                                                                                             14-DEC-1995;
                                                     10-0CT-1997
                                                                                                                                                         24-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                144;
                                                                                        Chitinase;
                                  AAW24554;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81
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The sequence given is encoded by the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this protein in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ||:::||| ||||||||| | | : ||||||||
krevaaflaqtshettggwatapdgpytwgycfkeenggagpdycggsagwpcaagkkyy 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- ATSPPYY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Region conserved between class I and class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chitinase; physical; biological; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 13; Length 336;
                                                                                                                                                                                                                                                             leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 747.5; DB 1
Pred. No. 8.8e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                II chitinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 33-34; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
123..323
   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           defence genes and selectable genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Scor
57.3%; Pred
tive 28; 1
standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92WO-US04282.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0704288
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                                                                                                                                                                        RCH10 chitinase protein.
                                                                                                                                                                                                                                     Promoter; region; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-415785/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ31407
                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-MAY-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-MAY-1991;
                                                                                                                 20-APR-1993
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Search completed: May
Job time: 7548 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The Sphi fragment of rice chitinase RCH10 gene (given in AAQ81346) and an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and Thanatephorus cucumeris fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-------ATSPPYY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 GRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 AGGAAAQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
190 grgpiglsynfnygpaggaigadllgdpdlvasdatvsfdtafwfwmtpgspkpscnava 249
                          185 LRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                      54.9%; Score 747.5; DB 16; Length 336; 57.3%; Pred. No. 9.8e-66; tive 28; Mismatches 63; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when grown in crops as a food source
                                                                                                                                                                                                                                                                             Chitinase; transgenic plant; disease resistance; crop improvement; tobacco; Nicotiana tabacum; plant defense; fungus pathogen; Cercospora nicotinae; Thanatephorus cucumeris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 31-32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maher EA, Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SALK ) SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                         AAR67969 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                            94WO-US07815.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    93US-0093372.
                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lamb CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-067090/09.
N-PSDB; AAQ81346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 142; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 336 AA;
                                                                                245 NLDCYTQR 252
                                                                                                      310 nldcysgr 317
                                                                                                                                                                                                                                                     Rice chitinase.
                                                                                                                                                                                                                                                                                                                                                Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1993;
                                                                                                                                                                                                                            13-AUG-1995
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310 310 314 314 302 302 302 373 148 3739 3739 3739 3739		ccation US/08162475A 44 TION: THIN: A novel endochi WITON: A novel endochi WITON: Tom the wild to THENCES: S ADDRESS: CUSHMAN, DARBY & CUSHM TON W YORK Avenue, N.W. Ington S.A. S.A. S.A. S.A. S.A. S.D. Nodel 30 TEM FC/2, Model 30 TEM FC/2, Model 30 TEM FC/2, Model 30 TEM FC/2, Model 30 WORDPERFOCK: S.A. S.S. inch, 720 kb dis S.S. inch, 720 kb dis S.S. inch, 720 kb dis T.S. S.	62 ty 63 ervativ	AVAAGGA : TGS
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		Application ormanication ormani	h Similarity 63.9%; 59; Conservative	ALAVCAAALLLAV
880000 8800000 88000000000000000000000		RESULT 1 RESULT 1 Sequence 5, Application US/08162475A Sequence 5, Application US/08162475A Patent No. 5656474 GENERAL INFORMATION: TITLE OF INVENTION: A novel endochitin TITLE OF INVENTION: induced by OSMOTION: TITLE OF INVENTION: from the wild tom TITLE OF INVENTION: from the wild tom CITY: Washington STREET: 1100 New YORK Avenue, N.W., CITY: Washington STREET: 1100 New YORK Avenue, N.W., ZIP: 20005-3918 CONNURY: U.S.A. ZIP: 20005-3918 COMPUTER READABLE FORM: ABDIUM TYPE: 3.5 inch, 720 kb diske OFFRAINS SYSTEM: PC-DOS 3.30 COMPUTER READABLE FORM: ABDIUM TYPE: 3.5 inch, 720 kb diske OFFRAING SYSTEM: PC-DOS 3.30 COMPUTER: IBM PS/2, Model 30 OPERATING SYSTEM: PC-DOS 3.30 SOFTWARE: U.S.A. APPLICATION NUMBER: US/08/162,475A FILING DATE: December 7, 1993 CLASSIFICATION NUMBER: BEW/3122/2 REGISTRATION NUMBER: 32011 REFERENCE/DOCKET NUMBER: PEW/3122/2 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION NUMBER: PEW/3122/2 TELEFRA: (202) 861-3000 TELEFRA: (202) 862-0944 INFORMATION FOR SEQ ID NO: 5: SEQUENCE: NICOLIANA OCHRIBAL SOURCE: NICOLIANA	itc 2a1	6 ALAVC 9 ALFCC
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Query Match 59.9%
Best Local Similarity 62.33
Matches 154; Conservative
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                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08162475A
Patent No. 556474
GENERAL INFORMATION:
APPLICANT: Zohreh Tabaeizadeh
TITLE OF INVENTION: A novel endochitinase gene
TITLE OF INVENTION: A novel endochitinase gene
TITLE OF INVENTION: Induced by osmotic stress and abscisic acid isolated
TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
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                                                                  RGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: December 7, 1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, Paul B. Jr.
REGISTRATION NUMBER: 32011
FERERNECE/COCKET NUMBER: PEW/3122/204351
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
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MBDIUM TYPE: 3.5 inch, 720 kb
COMPUTER: IBM PS/2, Mcdel 30
OPERATING SYSTEM: PC-DOS 3.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 December 7, 1993
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TELEFAX: (202) 822-0944
INFORMATION FOR SEC ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/
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NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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Matches 157;
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US-08-162-475A-2
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CITY: Wa
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TITLE OF INVENTION: A novel endochitinase gene
TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
TITLE OF INVENTION: induced by osmotic stress and abscisic acid isolated
TITLE OF INVENTION: from the wild tomato Lycopersicon chilense Dun.
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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                               11 AAALLLAVAAGGAAAQGYGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGF
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62.3%; Pred. No. 6.8e-79;
iive 30; Mismatches 56;
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ATTORNEY/AGENT INFORMATION:
NAME: White, Paul B. Jr.
REGISTRATION NUMBER: 32011
REPERENCE/COCKET NUMBER: PEW/3122/204351
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: (202) 861-3000
TELEPHONE: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: U.S.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM: ....TTM TYPE: 3.5 inch, 720 kb diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: Protein
; ORIGINAL SOURCE: Lycopersicon chilense
US-08-162-475A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/162,475A
                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08162475A; Patent No. 5656474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3.5 inch, 720 kb COMPUTER: IBM PS/2, Model 30 OPERATING SYSTEM: PC-DOS 3.30 SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       December 7, 1993
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APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNDAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNDAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
           PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRR 187
                                              188 WIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD
                                                                                                                                                       DB 3;
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PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%; Score 814.5; DB 362.1%; Pred. No. 1.1e-78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cornelissen, Bernardus J.C.
Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/647,831
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Murashige, Kate H. REGISTRATION NUMBER: 29,
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Palo Alto
California
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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Matches 154; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                               248 CYTQRNFA 255
                                                                                                                                                                                                                                                                                                   245 CYNORNEA 252
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US-08-229-050-9
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                               US-08-229-050-9
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STATE:
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                       128 1
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APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKBEISKATSPPYYGRG 127
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SOFTWARE PATENTING STATEM.
SOFTWARE PATENTING Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY-AGENT INFORMATION:
NAME: MURSHING MARTINGENERAL OF THE PATENTING PATES TO THE PATENTING PATES TO THE PATENT OF THE PATENTING PATES TO THE PATES TO THE PATENTING PATES TO THE PATES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                      Cornelissen, Bernardus J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sela-Buurlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                 Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1: Morrison & Foerster 755 Page Mill Road
                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08047413
Patent No. 5670706
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TELEFAX: 415-494-0792
TELEX: 706141
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Best Local Similarity 62.1%
Matches 154; Conservative
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STATE: California
COUNTRY: USA
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APPLICANT: Cornel
                                                                                                                                                 242 NNOKNFA 248
                                                                                          249 YTORNFA 255
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STREET: 753
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APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                                                                                                                                                                      RESULT 4
US-08-047-413-9
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LENGTH: 253
                                                                              Matches 154;
US-08-801-563-9
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                                                Query Match
Best Local
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APPLICANT: Melchers, Leo S.
APPLICANT: Wallenhoff, Elisabeth J.S.
APPLICANT: van Roekel, Jercem S.C.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Moloshuk, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Mithorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        PGFGTTGDDTARKKEIAAFFGQTSHETTGGTLSPDGPYAGGYCFLRE-GNQMGNGYYGRG 124
                                                                                                                  128 PIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRR 187
                                                  PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKBEISKATSPPYYGRG 127
                                                                                                                                                                                      188 WIPTAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYIRYCGMLGTAIGGNLD
 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/801,563
FILLIG DATE:
CLASSIFICATION: 600
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APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-AN-1991
ATTORNEY AGENT IRPORMATION:
NAME: MITCASHIGE, Kate H.
REGISTRATION NUMBER: 29,959
REGISTRATION NUMBER: 24,615-20022.00
TELEPHONE: 415-494-0792
TELEPHONE: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                           Cornelissen, Bernardus J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morrison & Foerster STREET: 755 Page Mill Road CITY: Palo Alto STATE: California COUNTX: USA ZIP: 94304-1018 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08801563
Patent No. 6087560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 254 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
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245 CYNQRNFA 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242
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                                       Gaps
                                                                                                                                                     68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                              WTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT 66
                                                                         8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF 67
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Length 254;
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                                       Indels
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61.0%; Pred. No. 4.9e-78;
iive 34; Mismatches 56;
59.8%; Score 814.5; DB 3;
62.1%; Pred. No. 1.1e-78;
ive 31; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: RAIKHEL, NALASHA V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSO 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0S-07-791-931-9;
Sequence 9, Application US/07791931C;
Patent No. 6133507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT; ORGANISM: Nicotiana tabacum
US-07-791-931-9
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                                           Conservative
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Matches 152; Conserv
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FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
LENGTH: 266
TYPE: PRI
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ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6271438
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STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kole, Lisa
REGISTRATION UNMBER: 35,225
REFERENCE/DOCKET NUMBER: A21
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 18,839
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TELER: (212) 765-2519
TELEX: 238555
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTER.STICS:
LENGTH: 266 amino acids
                                                                                                                                                                             ; ORGANISM: Hordeum vulgare US-07-791-931-10
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NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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RY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK---
                                                                                                                    Transgenic pathogen-resistant organism
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                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC competible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
                                                                                                             TITLE OF INVENTION: Transgenic pathogen-resistant on NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: KOLE, Lisa
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEPAS: (212) 765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Sequence 10, Application US/07791931C | Sequence 10, Application US/07791931C | Fatent No. 6133507 | GENERAL INFORMATION: APPLICAMN: RAIkhel, Natasha V. | TITLE OF INVENTION: Nettle Lectin CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/812,025 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 KRYCDILGVGYGNNLDCXSQRPFA 266
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                            Sequence 10, Application US/08812025 Patent No. 5804184 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TENGTH: 266 amin-
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Best Local Similarity 56.8%
Matches 150; Conservative
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MOLECULE TYPE: protein
US-08-812-025-10
                                                                                                                                                                                                                                                                                ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
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172 TAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYY 231
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                                                                                    6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                66 TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-----
                                                                                                                                                                                                           Transgenic pathogen-resistant organism
12
; DB 4; Length 266;
4e-74;
ches 69; Indels
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Query Match 56.7%; Score 772; DB Best Local Similarity 56.8%; Pred. No. 4e-7 Matches 150; Conservative 31; Mismatches
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RY: U.S.A.
90071-2921
                             Similarity
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US-08-093-372-2
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                                             Matches 142;
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             Query Match
                               Local
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                                                                                                                                                                                                                                                                                                                                     118 -----ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWM 171
                                                                                                                                                                                                                                                                                                                                                        172 TAQGNKPSCHNVALRRWIPTAADTAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYY 231
                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS
                                                                                                    Ouery Match 56.7%; Score 772; DB 4; Length 266; Best Local Similarity 56.8%; Pred. No. 4e-74; Matches 150; Conservative 31; Mismatches 69; Indels 14; Gaps
                                                                                                                                                                                                          3 SLAVVVAVVATVAMAIGTARGSVSSIVSRAQFDRMLLHRNDGACQAKGFYTYDAFVAAAA 62
                                                                                                                                                                                   6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
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APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 131
REFERENCE/DOCKET NUMBER: P31
RELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        232 TRYCGMLGTATGGNLDCYTQRNFA 255
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3:
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TELEFAX: (619) 546-9392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                             MOLECULE TYPE: protein
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TYPE: amino acid
TOPOLOGY: linear
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                                                   US-09-138-873A-10
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                                                                                    20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYIYDAFIAAANTFPGFGTIGSADDI 79
                                                  Gaps
                                                                                                                                                                                                                                                                                                                    185 LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG
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            Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08093372;
Patent No. 5530187;
GENERAL INFORMATION:
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Christopher J.
APPLICANT: Maher, Elleen A.
APPLICANT: Dixon, Richard A.
APPLICANT: Dixon, TRANSENIC PLANTS CONTAINING MULTIPLE TITLE OF INVENTION: TRANSENIC PLANTS CONTAINING MULTIPLE TITLE OF EXQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 747.5; DB 1;
57.3%; Pred. No. 2.2e-71;
Live 28; Mismatches 63;
Score 747.5; DB 1;
Pred. No. 2.2e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Pretty, Schroeder, Brueggemann & STREET: 444 South Flower Street, Suite 2000
  54.9%; Scor.
57.3%; Pred. No. 2.2.
'''e 28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 619-546-4737
619-546-9392
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: protein US-08-093-372-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 142; Conserva
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63 APIDLSALISRSTEDQMLKHRNDGACPAKGEYIYDAFIAAAKAYPSFGNTGDTATRKREI 122
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/07704288C
Patent No. 5399680
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 AAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDL 83
                                                                                                                                                                    125 GRGPIQLFGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNXPSCHNVA 184
                                                                                                                                                                                                                        185 LREWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                -ATSPPYY 124
20 AGGAAAQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTIGSADDI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.8%; Score 719; DB 1;
53.9%; Pred. No. 2.2e-68;
Live 37; Mismatches 64
                                                                           80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
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: United States
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STATE: California
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                                                                                                                                                                                                                                                                                                           245 NLDCYTQR 252
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                                                                                                                                                                                                    185 LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                                             Gaps
                                                   -ATSPPYY 124
                           20 AGGAAAQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTIGSADDI 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08379259
Patent No. 5695939
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: LEEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.9%; Score 747.5; DB 1
57.3%; Pred. No. 2.2e-71;
7ative 28; Mismatches 63
                                                                                                         80 KRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTATION NUMBER: 31,192
REPERBNOE/DOCKET NUMBER: P31
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
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Best Local Similarity 57.3
Matches 142; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 444 South
CITY: Los Angeles
STATE: California
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                   243 SADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGFFKRYCDLLGVGYGNNLDCYSQ 302
                                                                       132 IGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPT 191
----SPPYYGRGPIQL 131
                                                                                               SWNYNYGQCGRAIGVDLINKPDLVATDSVISFKSALWFWMTAQSFKPSSHDVITSRWTPS
                                                                                                                                                192 AADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles STATE: California COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 90071-2921

MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLANT DEFENSE GENES AND PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52.8%; Score 719; DB 1; 53.9%; Pred. No. 2.2e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
84 AAFFGQISHETIGGTRGAAD-QFQWGYCFKEEISKAT-
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: IAMB, CHRISTOPHER J.
APPLICANT: 2HJ, QUN
TITLE OF INVENTION: PEANT DEFENSE GENEE
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8899
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TELECOMNUNICATION INFORMATION:
TELEPHONE: (619) 546-9392
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/08379259
Patent No. 5695939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : California
RY: United States
90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-379-259-9
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TYPE: amino acid
STRANDEDNESS: unkr
TOPOLOGY: unknown
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Best Local Similarity
Matches 132; Conserv
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US-08-379-259-9
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                                                                                                                                             243 SADVAARRLPGYGTVTNIINGGLECGRGQDSRVQDRIGFFKRYCDLLGVGYGNNLDCYSQ 302
                                                          132 TGRSNYDLAGRALGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPT 191
                       123 AAFLGQISHETTGGWATAPDGPYAWGYCFVRERNPSTCSATPQFPCAPGQQYYGRGPIQI
                                                                              84 AAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISKAT--
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Job time: 745 sec
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C; Species: Hordeum vulgare (barley)
C; Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Accession: $48847
R; Bryngelsson, T; Collinge, D.B.; Green, B.; Gummesson, P.O.; Kragh, K.; Thordal-Chr submitted to the EMBL Data Library, March 1994
A; Description: Purification, characterization and cDNA sequence of a basic chitinase A; Reference number: $48847
A; Accession: $48847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 PPYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-256 < RRY>
A; Cross-references: EMBL:X78671; NID:9563486; PIDN:CAA55344.1; PID:9563487
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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C; Superfamily: plant chitinase; plant chitinase homology
C; Superds: glycosidase; hydrolase; polysaccharide degradation
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-256/Product: chitinase cht2a #status predicted <MAT>
F;31-255/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.9%; Score 1334; DB 2; Length 2
Best Local Similarity 98.4%; Pred. No. 2e-108;
Matches 252; Conservative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chitinase (EC 3.2.1.14) cht2a precursor - barley
                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                            T10802
S14948
T09687
JQ0965
T10810
S05426
                                                                                                                                                                                                     $57482
$20981
$65020
$65019
$08627
$43317
$56694
  T03239
S59947
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Copyright (c) 1993 - 2000
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Maximum Match 100%
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Post-processing:

rotal number of

Searched:

Title: Perfect score:

Sequence:

protein

Run on: W

Scoring table:

DB seq DB seq

Maximum Minimum

RESULT 2 848848 chithase (EC 3.2.1.14) cht2b precursor - barley C;Species: Hordeum vulgare (barley)

ATGGNLDCYTQRNFAS 256

241 241

δ q

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oblines (EC 3.2.1.14) chil7 precursor - tomato chitines (EC 3.2.1.14) chil7 precursor - tomato c;Species: Lycopersicon esculentum (tomato) c;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999 c;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999 c;Accession: 337342; S2635 A;Accession: S37342; S2635 A;Accession: S37342; Ail; WulD:99,03061 A;Accession: S37342 A;Accession: S37341; WulD:94,003061 A;Accession: S37342 A;Acc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.J.; Bol, J.F.; van Roekel, J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                          TPPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYG 125
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                                                                                6 ALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
SFPGFGTTGDDTARRKEIAAFFGQTSHETTGGSL-SAEPFTGGYCFVRQNDQ--SDRYYG 121
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A. Molecule type: mRNA
A. Residues: 1-253 CLIN>
A. Cross-references: EMBL:X51425; NID:919772; PIDN:CAA35789.1; E.
C. Superfamily: plant chittinase homology
C. Keywords: 91ycosidase; hydrolase; polysaccharide degradation
F) 30-251/Pomain: plant chitinase homology <PCH>
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ses 159; Conserv
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                        C; Date: 10-Dec-1994 #sequence_revision 10-Nov-1995 #text_cnange 26-044 #sequence_revision 10-Nov-1995 #text_cnange 26-044 #sequence_revision 10-Nov-1995 #text_cnange 26-044 #sequence_revision 11: Collinge, D.B.; Green, B.; Gummesson, P.O.; Kragh, K.; Thordal-Christ submitted to the EMBL Data Library, March 1994
A; Description: Purification, characterization and cDNA sequence of a basic chitinase from A; Recence number: 548847
A; Accession: 548848
A; Molecule type: mRNA
A; Residues: 1-222 <BRX>
A; Cross-references: EMBL:X78672; NID:9563488; PIDN:CAA55345.1; PID:9563489
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: A; Genetics: A; Genetics: C; Superfamily: plant chitinase; polysaccharide degradation
C; Superfamily: plant chitinase chit2b #status predicted <SIG>F; 1-22/Domain: signal sequence #status predicted <MAT>F; 23-252/Product: chitinase chit2b #status predicted <MAT>F; 27-251/Domain: plant chitinase homology <PCH>
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C; Species: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C; Date: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C; Accession: B34801
R; Payne, G; Ahl, P.; Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Eyals, C; Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A; Title: Isolation of complementary DNA clones encoding pathogenesis-related B; Reference number: A34801; MUID:90115914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYG 125
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                      10-Nov-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAAANTEPGEGTTGSADDIKRDLAAFFGGTSHETTGGTRGAADQFQWGYCFKEEISKATS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              252;
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Pred. No. 1.6e-102;
); Mismatches 5;
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64.3%;
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nilarity 93.0%;
Conservative 9
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Best Local Similarity
Matches 160; Conserv
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A; Residues: 1-253 <PAY>
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Matches 238; Conserv
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C; Species: Nicotiana tabacum (common tobacco)
C; Species: Nicotiana tabacum (common tobacco)
C; Species: 19-Peb-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C; Accession: $20737
R; Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meu submitted to the EMBL Data Library, January 1990
A; Description: Constitutive expression of acidic and basic Chitinase in transgenic to A; Reference number: $20737
A) Accession: $20737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYTRYCGMLGTATGGNL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chitinase (EC 3.2.1.14) pcht1 precursor - Lycopersicon chilense (fragment) N; Alternate names: endochitinase pcht1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR 126
        YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                     A, Molecule type: mRNA
A, Residues: 1-253 <LIN>
A, Cross-references: EMBL:X51426, NID:q19770, PIDN:CAA35790.1; PID:q19771
C, Superfamily: plant chitinase; plant chitinase homology
C, Keywords: glycosidase, hydrolase; polysaccharide degradation
F) 30-251/pomain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT
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61.4%; Pred. No. 1.2e-63;
wismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                     chitinase (EC 3.2.1.14) PR-P - common tobacco N;Alternate names: acidic chitinase PR-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             153; Conservative
                                                                                                                                                                                                                           241 ATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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A; Residues: 1-250 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 DCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCYNORNEA 251
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N.Alternate names: endochitimase pcht28
C;Species: Lycopersicon chilense
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 22-Jun-1999
C;Accession: S51589
R;Chan, R.D.; Yu, L.X.; Greer, A.F.; Cheriti, H.; Tabaeizadeh, Z.
Mol. Gen. Genet. 245, 195-202, 1994
A;Title: Isolation of an osmotic stress- and abscisic acid-induced gene encoding an acid A;Reference number: S51588; MUID:95115667
A;Accession: S51589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKBEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Molecule type: mRNA
A, Residues: 1-253 < CHE>
A, Cross-references: EMBL:L19342; NID:g437018; PIDN:AAA64999.1; PID:g767828
A, Cross-references: EMBL:L19342; NID:g437018; PIDN:AAA64999.1; PID:g767828
C; Genetics: A, Gene: pcht28
C; Superfamily: plant chitinase; plant chitinase homology
C; Superfamily: glycosidase; hydrolase
C; Superfamily: signal sequence #status predicted < SIG>
F; 1-24/Domain: signal sequence #status predicted < MAI>
F; 25-253/Product: chitinase #status predicted < MAI>
F; 30-251/Domain: plant chitinase homology < PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 GPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGIAIGGNL 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR 126
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A; Cross-references: EMBL: Z15139; NID: 919186; PIDN: CAA78844.1; PID: 919187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58 FPGFGTTGDDTARKKEIAAFFGQTSHETTGGSLSADGPFAGGYCFVREGNQMGS-GFYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MVLCCVFLLFLT---GSFAQDVGTIVTSDLFNEMLKNRNDDRCPAKGFYTYDAFIAAANS
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                                                                                                                                                                                                                                                                                                                                               Length 247;
                                                        A; Molecule type: protein
A; Residues: 112-115;183-188;218-221 <DA2>
C; Genetics:
A; Gene: chil7
C; Superfamily: plant chitinase; plant chitinase homology
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 1-16-70main: signal sequence #status predicted <SIG>
F; 17-247/Product: chitinase chil7 #status predicted <MAT>
F; 22-245/Domain: plant chitinase homology <PCH>
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61.6%; Pred. No. 1.4e-64;
live 32; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                       Query Match
62.4%; Score 850; DB 2;
Best Local Similarity 63.5%; Pred. No. 1.8e-66;
Matches 158; Conservative 34; Mismatches 53.
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Best Local Similarity 61.69
Matches 157; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 DCYDQRNFA 245
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A34801
pathogenesis-related protein P precursor - common tobacco
c)Species: Nicotiana tabacum (common tobacco)
c)Species: Nicotiana tabacum (common tobacco)
c)Species: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 22-Jun-1999
C)Accession: A34801
R;Payne, G;Ahl, P: Moyer, M.; Harper, A.; Beck, J.; Meins Jr., F.; Ryals, J.
Proc. Natl. Acad. Sci. U.S.A. 87, 98-102, 1990
A;Title: Isolation of complementary DNA clones encoding pathogenesis-related proteins
A;Reference number: A34801; MUID:90115914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the hydrolysis of the beta-1,4-N-acetyl-D-glucosamine linkag hydrolase
                                                                                                                                                                                                                                                                                                                               C, Accession: T03017
R; Kim, C.Y.; Gal, S.W.; Choe, M.S.; Jeong, S.Y.; Lee, S.I.; Cheong, Y.H.; Lee, S.H.; Plant Mol. Biol. 37, 523-534, 1998
A; Title: A new class II rice chitinase, Rcht2, whose induction by fungal elicitor is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: Decliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-175 <KIM>
A;Residues: 1-175 <KIM>
A;Cross-references: EMBL:L40338; NID:g2340042; PIDN:AAC37516.1; PID:g2340043
A;Experimental source: cv. Cheongcheongbyeo
C;Function:
A;Description: catalyzes the hydrolysis of the beta-1,4-N-acetyl-D-glucosamin
C;Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                  C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 DLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           142 RAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LFCCVFFLFLT---GSLAQGIGSIVINDLFNEMLKNRNDGRCPANGFYTYDAFIAAANS 65
185 WIPSAADISANRVPGYGVIINIINGGIECGKGQNARVEDRIGYYRRNVSIMNVAPGDNLD 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 GYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS 256
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                                                                                                                                                                                                                               probable chitinase (EC 3.2.1.14) class II - rice (fragment) N,Alternate names: class II acidic chitinase; Rcht2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.4%; Score 808.5; DB 2; 61.0%; Pred. No. 7.5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.8%; Score 814; DB 2; I ilarity 83.4%; Pred. No. 1.7e-63; Conservative 13; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Reference number: 214820; MUID: 98278381
A, Accession: T03017
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Best Local Similarity 61.0%
watches 152; Conservative
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A; Residues: 1-253 <PAY>
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                                                                                                       252
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                                                                                       248 CYTORNEA
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Best Local Simil
Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
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N;Alternate names: acidic chitinase
C;Species: Petunia x hybrida (garden petunia)
C;Species: Petunia x hybrida (garden petunia)
C;Species: Petunia x hybrida (garden petunia)
C;Accession: $20.741
R;Linthorst, H.J.M.; van Loon, L.C.; van Rossum, C.J.; Bol, J.F.; van Roekel, J.; Meulen submitted to the EMBL Data Library, January 1990
A;Reference number: $20.737
A;Reference number: $20.737
A;Reference number: $20.737
A;Residues: 1-254 <LIN>A;Residues: 1-254 <LIN>A;Residues: Data Chitinase homology
C;Superferences: EMBL:X51427; NID:g20503; PIDN:CAA35791.1; PID:g20504
C;Superferences: Plant chitinase; plant chitinase homology
C;Reywords: glycosidase; hydrolase; polysaccharide degradation
F;29-252/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ij
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTPTAADTAAGRVPQYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLD 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 PGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGFGTTGDDTARKKEIAAFFGQTSHETTGGTLSPDGPYAGGYCFLRE-GNQMGNGYYGRG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              189 TPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDC 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 GTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQ 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRW 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29
       A;cross-references: EMBL:M97210; NID:g310936; PIDN:AAA64998.1; PID:g767827
C;Genetics:
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVLALSEVVELELIGILAQNVGSIVISDLEDQMLKNRNDARCFAVRFYIYDAFIAAANSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 AAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGF
                                                                                                                                                                                                                                                                                                                                                                                                                         7 ALSCLFFLFLTGTLAQNAGSIVTRELFEQMLSFRNNDACPAKGFYTYDAFIAAANSFPGF
                                                                                                                                                                                                                                                                                                                    7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254;
                                                                                                                                                                                                                                                                  Length 250;
                                                                                                                                          <SIG>
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                                                                                                                                                                                                                                                                                                                         Indels
                                                               A; Gene: pchtl
C; Superfamily: plant chitinase; plant chitinase homology
C; Kaywords: glycosidase; hydrolase
F; 1-21/Domain: signal sequence (fragment) #status predicted
F; 22-250/Product: chitinase #status predicted <MAT>
F; 27-248/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                    Score 816.5; DB 2;
Pred, No. 1.5e-63;
30; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.8%; Score 814.5; DB 2
llarity 62.1%; Pred. No. 2.3e-63;
Conservative 31; Mismatches 62
                                                                                                                                                                                                                                                                       59.9%;
62.3%;
                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 154; Conserv
                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      249 YTQRNFA 255
                                                                                                                                                                                                                                                                                                                         154;
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Best Local S:
Matches 154
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Savetal Saveta
A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu A;Reference number: S37341; MUID:94003061
A;Accession: S37343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 HNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AANSFPGFGTAGDDTARKKEIAAFFGQTSHETNGGSAGT---FTGGYCFVKQIEQ--SDR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 YYGRGPIQLIGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-233 <DAN>
A;Cross.references: EMBL:215141; NID:g19188; PIDN:CAA78846.1; PID:g19189
A;Accession: S38839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 AALVALAVLAAALATAARAEQCGAQAGGARCPNCLCCSRWGWCGTTSDFCGDGCQSQCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTXDAFIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 253;
                                                                                                                                                                                                                                                                             A,Gene: chi3
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;124/Domain: signal sequence. #status predicted <MAI>F;25-253/Product: chitinase chi3 #status predicted <MAI>F;30-251/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 797.5; DB 2; 50.3%; Pred. No. 9.4e-62; iive 28; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.0%; Score 803.5; DB 2; 59.2%; Pred. No. 2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 ARFAALAVCAAALLLA-----VAAGGA-
                                                                                                                                                                                              A,Molecule type: protein
A,Residues: 134-152;225-228 <DA2>
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 59.2%
Matches 151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 PTGENLDCNNOKNFA 251
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Best Local Similarity
Matches 162; Conserv
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C;Species: Lycopersicon esculentum (tomato)
C;Date: 31-Dec-1993 *sceluence_revision 31-Dec-1993 *text_change 22-Jun-1999
C;Accession: S37343; S38839; S25636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 SKATSPP----YYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWF 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AANTFPGFGTTGSADDI--KRDLAAFFGQTSHETTGGTRGAADQFQWGYCF----KEEI 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 WMTAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIG 229
                                                                                                                           GPIQLIGRSNYDLAGRALGKDLVSRPDLVSTDAVVSFRTAMWFWMTAQGNKFSCHNVALR 186
                                                                                                                                                          RWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNL 246
                                                                                                                                                                                                                                                                183 SWIPSAADQSANRAPGCGVITNIINGGIECGVGPNAAVEDRIGYXRRYCGMLNVAPGDNL 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 95/1; 143/2
C;Superfamily: plant chitinase; plant chitinase homology
C;Keywords: glycosidase; hydrolase
F;30-264/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 59.1%; Score 805.5; DB 2
Best Local Similarity 57.4%; Pred. No. 1.4e-62;
Matches 152; Conservative 35; Mismatches 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chitinase (EC 3.2.1.14) class II - peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         230 YYTRYCGMLGTATGGNLDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 FYKRYCDILKIGYGSNLDCANQOHF
                                                                                                                                                                                                                                                                                                                                                  DCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                 DCYNORNFA 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: chi2.2
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S37343
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RESULT 15
839979
chitimase (EC 3.2.1.14) - rice
C;Species: Oryza sativa (rice)
C;Accession: S39979
R;Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen Genet. 241, 1-10, 1993
A;Title: Sequence variation, differential expression and chromosomal location of rice cha;Reference number: S39979; MuID:94049667
A;Reference rumber: S39979; MuID:94049667
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-339 cris.
A;Cross-references: EMBL:X56787
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;33-74/Domain: hevein chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         250 GNKPSSHDVITGRWAPSPADAAAGRAPGYGVITNIVNGGLEGGHGPDDRVANRIGFYQRY 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24 -----AAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSAD 77
                                                                     190 WPCAPGRKYYGRGPIQLSFNFNYGPAGRAIGVDLLSNPDLVATDATVSFKTALWFWATPQ 249
74 CGPTPTPPSPSDGVGSIVPRDLFERLLLHRNDGACPARGFYTYEAFLAAAAAFPAFGG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 ALAVLAAALATAARAEQCGAQAGGARCPNCLCCSRWGWCGTTSDFCGDGCQSQCSGCGPT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----YYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQ
                                                                                                                                                                                             GNKPSCHNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 DIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISKATSPP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                        TGSADDIKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKBEISKATSPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.4%; Score 795; DB 2; L. 50.8%; Pred. No. 1.5e-61; Live 28; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 ALAVCAAALLLA-----VAAGGA-~
                                                                                                                                                                                                                                                                          CGMLGTATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                      CGAFGIGTGGNLDCYNQRPFNS 331
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Search completed: May 3, 2002, 18:32:10 Job time: 7473 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein May 3, 2002, 18:33:16 ; Search time 78.59 Seconds (without alignments) 119.432 Million cell updates/sec Run on:

US-09-534-229C-1 1362 1 MARFAALAVCAAALLIAVAA.....MIGTATGGNLDCYTQRNFAS 256 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 seqs, 36664827 residues Searched: 100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		514	Q05540 Lycopersico	Q40114 lycopersico	petur	P17513 nicotiana t	lycopers	nordeum v	orassica	_	arabido	oryza	vitis vin	P36907 pisum sativ	Q39799 gossypium h	P24626 oryza sativ	P06215 phaseolus v	Q41596 theobroma c	phaseolu	gossypiu	P05315 solanum tub	nicotian	nicotian	01	solanum	P08252 nicotiana t	P52405 solanum tub	P21226 pisum sativ	lycopers	Q05537 lycopersico	snindod	solanum		snindod
SUMMARIES	F		CHIQ_TOBAC	CHIB_LYCES		CHIT_PETHY	CHIP_TOBAC	CHIA_LYCES	CHI2_HORVU	CHI2_BRANA	CHI1_HORVU	CHIT_ARATH	CHI2_ORYSA	CHIB_VITVI	CHIX_PEA	CHI1_GOSHI	CHI1_ORYSA	CHIT_PHAVU	CHI1_THECC	CHI5_PHAVU	CHI2_GOSHI	CHIT_SOLTU	CHI3_TOBAC	ı	CHI2_SOLTU	CHI1_SOLTU	CHI1_TOBAC	CHI3_SOLTU	CHI2_PEA	CHIC_LYCES	CHID_LYCES	CHI6_POPTR	1	_ا	CHI8_POPTR
	מת אדאמם ד	,	33																							~	•	~	_	C)	10	_	~	303 1	LO.
	& Query Match Lo	ו וני	62.7	62.4	60.8	59.8	59.4	59.0	56.7	56.4	55.4	55.1	54.9	54.3	53.1	53.1	53.0	52.8	52.7	52.2	52.2	52.1	52.0	51.8	51.8	51.8	51.5	51.3	51.3	50.8	CD.	m	47.3	45.1	41.6
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AGI_URTDI CHIP BETVU	CHIB_MAIZE	CHI4_PHAVU	CHI4_BKANA CHIT_DIOJA	CHI4_ARAHY	CHIB_ARAHY	CHI3_ARAHY	IAMY_COILA
~ ~			⊣ ⊢	Н.		Η.	H
372	269	270	250	46	446	46	133
34.8	27.0	27.0	25.0 24.6	14.6	14.2	13.4	13.3
474	380.5	367.5	340.5	199	194	183	181
3.4 4.4	986	7 80 10 00	ω 4 ον Ο	4.	4 4 4 0	44	45

ALIGNMENTS

us-09-534-229c-1.rsp

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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                      185
                                                                                                                                                                                                                                                                                                                                                                                       RRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                     182 GRWTPSAADQAANRVPGYGVIINIINGGIECGIGRNDAVEDRIGYYRRYCGMLNVAPGEN 241
                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                 6 ALAVCAAALILLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                         64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLANCE MOLITHMIC THE ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST CHITINA CONTAINING FUNCAL PARTHOGENS.

-!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNCAL PARTHOGENS.
-!- CATALYTIC ACTIVITY: HYDROKYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAINE POLIMERS OF CHITIN.
-!- KNOCHITON: BY FUNCAL INFECTIOLAR.
-!- INMICATION: BY FUNCAL INFECTION.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-BIDDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Būkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.: "Molecular characterization of four chitinase cDNAs obtained from Cladosporium fulvum-infected tomato.";
                                                                                                                                                                                                                                                 9 ALFCCVFFLFLT----GSLAQGIGSIVTSDLFNEMLKNRNDGRCPANGFYTYDAFIAAAN
                                                                                                                                                                                                                                                                                                    SPPGFGTTGDDTARRKEIAAFFGQTSHETTGGSL-SAEPFTGGYCFVRQNDQ--SDRYYG
                                                                                                                                                                                                                                                                                                                                      RGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND SEQUENCE OF 112-115; 182-188 AND 218-221
                                                                                                                                                                              Length 253;
                                                                                                                                                                                                         Indels
                                                                                                                ACIDIC ENDOCHITINASE Q.
Y -> F (IN STRAIN SAMSUN).
ODED41DEA99CE196 CRC64;
                                                                           Pathogenesis-related protein; Hydrolase; Glycosidase;
Chitin degradation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-CCT-1994 (Rel. 30, Last annotation update)
ACIDIC 27 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                 DB 1;
                                                                                                                                                                              62.7%; Score 854.5; DB 1
64.3%; Pred. No. 3.7e-64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247 AA
                                                                                                                                                                                                         Mismatches
  HSSP; P23951; 2BAA.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. MONEYMAKER;
MEDLINE=94003061; PubMed=8400122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                         32;
                                                                                                                253 AK
54 Y
27632 MW;
                                                                                                                                                                                  Query Match 62.77
Best Local Similarity 64.33
Matches 160; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                               54
253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 LDCYNORNF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                            LDCYTQRNF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHIB_LYCES
Q05540;
                                                                                                                                               SEQUENCE
                                                                                                                                VARIANT
                                                                                                         SIGNAL
                                                                                                                     CHAIN
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 FPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGR 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eŭkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MVLCCVFLLFLT---GSFAQDVGTIVTSDLFNEMLKNRNDDRCPAKGFYTYDAFIAAANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 850; DB 1; Length 247;
Pred. No. 8.5e-64;
1; Mismatches 53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACIDIC 27 KDA ENDOCHITINASE. C1163ED1D272A5E5 CRC64;
                                                                                                                                                                                                 PIR; S37342; S37344.

HISP, P23951; S37342.

InterPro; IPR000726; Glyco_hydro_19.

Pron; P00102; Glyco_hydro_19; 1.

ProDom; P0000574; Glyco_hydro_19; 1.

PROSITE; PS00774; CHITINASE_19_1; 1.

PROSITE; PS00774; CHITINASE_19_2; 1.

Pathogenesis-related protein; Hydrolase; Glycosidase; Chitin degradation; Signal.

SIGNAL

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIA_LYCCI STANDARD; PRT; 253 AA.
Q40114: Q40113;
01-N0V-1997 (Rel. 35, Created)
01-N0V-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ACIDIC ENDOCHITINASE PORTZE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: EXTRACELLULAR. INDUCTION: BY OSMOTIC STRESS AND ABSCISIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.4%; Score v...
63.5%; Pred. No. 8.5e-
+ive 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon chilense (Solanum chilense)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247 AA; 26583 MW;
                                                                                                                                                                                      EMBL; Z15139; CAA78844.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 62.43
Best Local Similarity 63.53
Matches 158; Conservative
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DCYDORNFA 245
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Nicotiana tabacum (Common tobacco)
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                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 AANSFPGFGTTGDDTARKKEIAAFFGQTSHETKGGSAGT---FTGGYCFVRQIDQ--SDR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 YYGRGPIQLIGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACIDIA EMPAIGA (PETUNIA).
Petunia hybrida (Petunia).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, endicotyledons, core eudicots,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 HNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TUCLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITINBINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                               R MBL; M97210; AAA64998.1; -
R HSSP; P23951; ZBRA.
R HSSP; P23951; ZBRA.
R HSSP; P23951; ZBRA.
R InterPro; IPR000726; Glyco_hydro_19.
R Profolus; Glyco_hydro_19; 1.
R PROSITE; PS00773; CHITINASE_19_1; 1.
R PROSITE; PS00774; CHITINASE_19_2; 1.
R PROSITE; PS00774; CHITINASE_19_2; 1.
R Hydrolase; Glycosidase; Chitin deradation; Signal.
SIGNAL 25 253 ACIDIC ENDCHITINASE PCHT28.
T CONFLICT 94 94 K -> N (IN REF. 1; AAA64998).
T CONFLICT 170 171 QD -> HH (IN REF. 1; AAA64998).
SEQUENCE 253 AA; 27569 MW; D48C269D5A794E60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermātophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; euasterids I; Solanales; Solanaceae; Petunia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.8%; Score 828.5; DB 1; 61.6%; Pred. No. 5.4e-62;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
ACIDIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           254 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32; Mismatches
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                                                                                                                                                                                                                                                                                                                                       EMBL; L19342; AAA64999.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 ATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 PTGENLDCNNOKNFA 251
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                                                                                       HYDROLASES)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157;
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AC CHIT_P
DT CHIT_P
DT 01-DEC
DT 01-DEC
DT 01-DEC
OC ENKARY
OC SPERMIN
OC ASTERI
CO A
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bol J.F., van Roekel J., Meulenhof J., Conelissen B.J.C.;
"Analysis of acidic and basic chitinases from tobacco and petunia and
their constitutive expression in transgenic tobacco.";
Mol. Plant Microbe Interact. 3:255-258(1990).
-!-FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST
CHITIN CONTAINING FUNGAL PATHOGENS.
-!-CATALYTIC ACITIVITY: HYDROLYSIS OF THE J.4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!-STUCKLICIAR LOCATION: EXTRACELLULAR FULUD FROM LEAVES.
-!-STUCKLICIAR LOCATION: EXTRACELLULAR FULUD FROM LEAVES
-!-STUCKLICIAR LOCATION: EXTRACELLULAR FULUD FROM LEAVES
-!-STUCKLICIAR LOCATION: EXTRACELLULAR FULUD ENDING LEAVES
-!-STUCKLICIAR LOCATION: EXTRACELLULAR FULUD ENDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127
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01-A03-1990 (Rel. 15, Last sequence update)
01-BDC-1992 (Rel. 24, Last annotation update)
ACIDIC ENDOCHITINASE P PRECURSOR (EC 3.2.1.14) (PATHOGENESIS-RELATED PROTEIN P) (PR-P).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WIPTAADTAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTAIGGNLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SVLALSEVVFLFLTGTLAQNVGSIVTSDLFDQMLKNRNDARCFAVRFYTYDAFIAAANSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.8%; Score 814.5; DB 1; Length 254; 62.1%; Pred. No. 7.8e-61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; PF00182; Glyco_hydro_19.

Probom; PF00182; Glyco_hydro_19; 1.

Probom; PF00187; Glyco_hydro_19; 1.

PROSITE; PS00773; CHITINASE_19_1; 1.

PROSITE; PS00774; CHITINASE_19_2; 1.

PRADAGENESIS-related protein; Hydrolase; Glycosidase; Chitin degradation; Signal.
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377F494721B1E29B CF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        254 A
27665 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X51427; CAA35791.1; -. EMBL; A16118; CAA01262.1; -. PIR; S20741; S20741. HSSP; P23951; ZBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      154; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                      HYDROLASES).
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ID CHIP_T
AC P17513
AC 01-7513
DT 01-AUG
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DE ACIDIC
OS NICOTII
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RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
EMBL; Z15141; CAA78846.1; -.
PIR; S37343; S37343.
HSSP, P23951; ZBAA.
InterPro; IPR000726; Glyco_hydro_19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00182; Glyco-hydro_19; 1.
Probon; PD00574; Glyco-hydro_19; 1.
PROSTIE; PS00773; CHITINASE_19_1; 1.
PROSTIE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35;
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253 AA;
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nes 151;
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Q05539;
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CHIA_LYCES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 GPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PERAIN=CV. SAMSUN: IISSUD=Leaf;
MEDLINE-2033079; PubMed=2131096;
Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,
Linthorst H.J.M., van Loon L.C., van Rossum C.M.A., Mayer A.,
Landlysis of acidic and basic chitinases from tobacco and petunia and
their constitutive expression in transgenic tobacco.";
MAND: Plant Microbe Interact. 3:252-258(1990).
-i- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST
                                                                                                                                                                                                                                                                                                    "Isolation of complementary DNA clones encoding pathogenesis-related proteins P and Q, two acidic chitinases from tobacco."; Proc. Natl. Acad. Sci. U.S.A. 87:98-102(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHITIN CONTAINING FUNGAL PATHOGENS.
-:- CATALYTIC ACTIVITY: HYDROLYGIS OF THE 1,4-BETA-LINKAGES OF
--- N-ACETYL-D-GLICOSAMINE POLYMERS OF CHITIN.
--- SUBCELLULAR LOCATION: EXTRACELLULAR FLUID FROM LEAVES.
-:- INDUCTION: DURING LOCAL NECROTIC RESPONSE TO THE TOBACCO MOSAIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FPGFGTSGDDTARRKEIAAFFGQTSHETTGGSL-SAEPFTGGYCFVRQNDQ--SDRYYGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LFCCVFFLFLT----GSLAQGIGSIVTNDLFNEMLKNRNDGRCPANGFYTYDAFIAAANS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO CLASS IA IN THE CAFALYTIC PART BUT LACK A N-TERMINAL CHITINBINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 253;
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, M29869; AAA34106.1; -.
EMBL, X51426; CAA35790.1; -.
PIR; A34601; A34801.
PIR; S20737; S20737.
INTERPO; IPR000726; Glyco_hydro_19.
Probom: PF00182; Glyco_hydro_19; I.
Probom: PF00182; Glyco_hydro_19; I.
PROSITE; PS00773; CHITINASE_19_1; I.
PROSITE; PS00774; CHITINASE_19_2; I.
PRATHOR PATHOR PROBLES OF CONTRIBUTION OF CONTRIBUTI
                                                                                                                                                                                                                          Payne G., Ahl P., Moyer M., Harper A., Beck J., Meins F. Ryals J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACIDIC ENDOCHITINASE P.
C -> Y (IN STRAIN SAMSUN).
AA49930C0A0C3E50 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 2.5e-60
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                                                                                                                                                               AND PARTIAL SEQUENCE
                                                                                                                                                               SEQUENCE FROM N.A., AND PARTIAL S:
STRAIN-CV. XANTHI NC;
MEDLINE-90115914; Pubmed-2296608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34;
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SIGNAL 1 24
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Best Local Similarity
Matches 152; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                     NCBI_TaxID=4097;
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                              Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
"Molecular characterization of four chitinase cDNAs obtained from Cladosporium filvum-infected formato.",
Plant Mol. Biol. 22:1017-1029(1993).
-!- FUNCTION: THIS ACIDIC CHITINASE FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNCAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
RWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: EXPRACELLULAR.
-!- INDUCTION: BY FUNGAL INFECTION.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IB WHICH IS SIMILAR TO CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Spermātophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBI_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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ACIDIC 26 KDA ENDOCHITINASE.
6C78CA3750DE6D7A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEGUENCE FROM N.A., AND SEQUENCE OF 134-152 AND 225-228
STRAIN=CV. MONDYMAKER,
MEDLINE=94003061; PubMed-8400122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pathogenesis-related protein; Hydrolase; Glycosidase; Chitin degradation; Signal. BY SIMITARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ACIDIC 26 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                    253 AA.
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                                        122
                                                                                         YYGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                             01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1992 (Rel. 21, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
26-AUG-2001 (Rel. 40, Last sequence (E 3.2.1.14) (CHI-26).
Hordeum vulgare (Barley).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
NCBL_TaxID=4513;
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E
                                                                                                                                                          AANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPP
                                                         J. Mol. Biol. 229:189-193(1993).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNCAL PATHOGENS.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINASE CLEASS IB WHICH IS SIMILAR TC
CLASS IA IN THE CATALYTIC PART BUT LACK A N-TERMINAL CHITIN-
BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                           HNVALRRWTPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
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Hart P.J., Monzingo A.F., Ready M.P., Ernst S.R., Robertus J.D.;
"Crystal structure of an endochitinase from Hordeum vulgare L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leah R., Tommerup H., Svendsen I., Mundy J.;
Blochemical and molecular characterization of three barley seed
"Blochemical and Information properties.";
proteins with antifungal properties.";
J. Biol. Chem. 266:1564-1573(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leah R., Mikkelsen J.D., Mundy J., Svendsen I.; "Identification of a 28,000 dalton endochitinase in barley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [2]
PRELIMINARY SEQUENCE OF 24-77 AND 148-188.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carlsberg Res. Commun. 52:31-37(1987).
                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. PIGGY;
MEDLINE=91107649; PubMed=1899089;
                                                                                                                                                                                               ATGGNIDCYTQRNFA 255
                                                                                                                                                                                                              || || || || || || PTGENLDCNNQKNFA 251
                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ALAVCAAALLLAVAAGGAAAQGYGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAAN 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                    Hydrolase; Glycosidase; Chitin degradation; Signal; 3D-structure.
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AA SEQUENCE)
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                                                                                                                                                                                                                                                     26 KDA ENDOCHITINASE
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56.8%; Pred. No. 2.8e-57;
iive 31; Mismatches 69;
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                                                                                                                                      Prodom; P0000574; Glyco_hydro_19; 1. PROSITE; PS00773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                 PDB; 2BAA; 15-JAN-96.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; 1.
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EMBL; L34210; AAA56786.1;
EMBL; M62904; AAA32941.1;
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                                            PIR; A29104; A29104.
PIR; A38664; A38664.
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Best Local Simi
Matches 150;
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CHIL_HORVU
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                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
Glycosidase; ChiLin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                            Hamel F., Bellemare G.;

"Nucleotide sequence of a Brassica napus endochitinase gene.";

Plant Physiol. 101:1403-140319393,

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF

N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHIIN.

-!- SIMILARITY: BELONGS TO CHIIINASE CLASS IA WHICH IS SIMILAR TO

CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL

CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.4%; Score 768; DB 1; Length 322; 58.4%; Pred. No. 7.3e-57;
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Y SIMILARITY
X SIMILARITY
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E62EB4B17211DBCD CRC64;
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CHITIN-BINDING (BY S
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                01-0cT-1994 (Rel. 30, Created)
01-0cT-1994 (Rel. 30, Last sequence update)
10-0cT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                    AA.
                                                                                                                                                  322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001002; Chitin_bind.
Interpro; IPR0001002; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000543; CHITINBINDNG.
ProDom; PD000509; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD000609; Chitin_bind; 1.
SMARY; SM0270; ChtBB1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=94143492; PubMed=8310072;
                                                                 243 KRYCDILGVGYGNNLDCYSQRPFA 266
                                              232 TRYCGMLGTATGGNLDCYTQRNFA 255
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Best Local Similarity 58.4%
Matches 142; Conservative
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                               Brassica napus (Rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
21
23
32
37
56
32 AA;
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Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASES).
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CHI2_BRANA
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5

14; Gaps

55; Indels

Mismatches

32;

28 VGSVIIRSVYASMLPNRDNSLCPARGFYIYDAFIAAANTFPGFGTIGSADDIKRDLAAFF 87

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                                                                                                                                                                                                                          251 DRAAGRVPGYGVITNIINGGLECGRGQDARVADRIGFYQRYCNILGVNPGGNLDCYNORS 310
                                                                                                                      134 RSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAA 193
                                                                                                                                           88 GQTSHETTGGTRGAAD-QFQWGYCFKEEISK------ATSPPYYGRGPIQLTG 133
                                                                 71 LSGIISRSQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPGFGTTGDTATRKKEIAAFF 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             [2]
SEQUENCE OF 141-318 FROM N.A.
STRAIN-CV. HIMALAYA;
STRAIN-CV. Huang J.-K., Lee G., Muthukrishnan S.;
"Identification of an endochitinase cDNA clone from barley aleurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-:- CATALITYIC ACTUTY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- INDUCTION: BY ETHYLENE.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                     DTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEGUENCE FROM N.A. STRAIN-GV. NK 15ST TISSUE-Leaf; STRAIN-GV. NK 15ST TISSUE IS INSTANCT. Huang J., Muthukrishnan S.; Ignatius S.,, Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
26 KDA ENDOCHITINASE I PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                 318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U02287; AAA18586.1; --
EMBL: X15349; CAA33407.1; --
FIR; S04131; S04131.
HSSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRIMTS; PR00451; CHITINBINDNG.
PRODOM; P000054; Glyco_hydro_19; 1.
ProDom; PD000654; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4513;
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FVN 315
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                                                                                                                                                                                                                                                                                                                                       181 APGKSYYGRGPIQLSHNYNYGPAGRAIGVDLLRNPDLVATDPTVSFKTAMWFWMTAQAPK 240
                                                                                                                                                                                                                                                                                                                                                                     241 PSSHAVITGQWSPSGTDRAAGRVPGFGVITNIVNGGIECGHGQDSRVADRIGFYRRYCDI 300
                                                                                                                                                                                                                                                                                           178 PSCHNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGM 237
                                                                                                                                                                                                                                                           120
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                                                                                                                                                                                Gaps
                                                                                                                                                                                                  26
                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                         71
SMART; SM00270; ChtBD1; 1.
PROSITE: PS00773; CHITINASE 19_1; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Multigene family.
SIGNAL
1 19 POTENTIAT.
                                                                                                                                                                                                                                                   1 MRAFVLFAVVAMAATMAVAEQCGSQAGGATCPNCLCCSRFGWCGSTPYCGDGCQSQCSGC
                                                                                                                                                                                                                                         --------GVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFG
                                                                                                                                                                                                                                                                               72 TIGSADDIKRDLAAFFGQISHETIGGIRGAAD-QFQWGYCFKEEISK-------
                                                                                                                                                                                                                                                                                                                     118 ATSPPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;
Samac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.;
"Isolation and characterization of the genes encoding basic and
acidic chitinase in Arabidopsis thaliana.";
Plant Physiol. 93:907-914(1990).
                                                                                                                                                                                63;
                                                                                                                                                            Length 318;
                                                                      26 KDA ENDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                71; Indels
                                                                                                            SIMILARITY.
SIMILARITY.
42D62B2FE8041954 CRC64;
                                                                                                                                                            DB 1;
                                                                                                                                                           55.4%; Score 754.5; DB 1
48.1%; Pred. No. 9.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1990 (Rel. 16, Created)
01-FPB-1991 (Rel. 17, Last sequence update)
01-FDB-1998 (Rel. 36, Last annotation update)
BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       322 AA.
                                                                                          SIMILARITY.
                                                                                                                                                                                31; Mismatches
                                                                                                                                                                                                    1 MARFAALAVCAAALLLAVA-----AGGAAAQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. COLUMBIA;
MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                     238 LGTATGGNLDCYTQRNFA 255
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318
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33402 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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318 AA;
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                                                                                 DOMAIN
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           134 RSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRWTPTAA 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTAIGGNLDCYTQRN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 DRAAGRLPGYGVITNIINGGLECGRGQDGRVADRIGFYQRYCNIFGVNPGGNLDCYNQRS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---ATSPPYYGRGPIQLTG 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLAAFF 87
                                       Chitin degradation; Chitin-binding; Signal.
Res. 7:217-221(2000).
FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REMOVED IN MATURE FORM (PROBABLE) CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.1%; Score 751; DB 1; Length 322; 56.8%; Pred. No. 1.9e-55; Live 35; Mismatches 56; Indels
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7 SIMILARITY.
7 SIMILARITY.
7 SPAFFE4C544FCCD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC ENDOCHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GQTSHETTGGTRGAAD-QFQWGYCFKEEISK---"--
                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M38240; AAA32769.1; ALT_INIT.
EMBL, AP002047; BAB03157.1; -
HSSP, 129351; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00726; Glyco_hydro_19.
Pfam; PF00182; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19.
PRINTS; PR00451; CHITINBINDIG.
PRODOM; PD000574; Glyco_hydro_19; 1.
PROSTIE; PS00070; Chitin_bind; 1.
PROSTIE; PS00070; CHITIN_BINDIG; 1.
PROSTIE; PS00773; CHITINASE_19_1; 1.
PROSTIE; PS00773; CHITINASE_19_1; 1.
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316
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23
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37
37
32 AA;
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Best Local S
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PROPEP
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250 IGGWIPSADDQRAGRVPGYGVITNIINGGLECGHGEDDRIADRIGFYKRYCDILGVSYGA 309
                                                                                                                                                                               STANDARD;
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61
61
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             314 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Multigene family. SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                               245 NLDCYTQR 252
                                                                                 310 NLDCYSQR 317
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=29760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROLASES).
                                                                                                                                                                               CHIB_VITVI
P51613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                challenge.
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                                                                                                                                                             CHIB_VITVI
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DR HSSP, S15997.

DR HSSP, S23951; 2BAA.

DR InterPro; IPR001002; Chittin_bind.

DR InterPro; IPR00126; Chittin_bind.

DR Prom; Pr00182; Chittin_binding; 1.

DR PRINTS; PR00451; CHITINBINDNG; 1.

DR Probom; PR000669; Chitin_bind; 1.

DR PROSTIE; PS00026; CHITINBINDNG; 1.

DR PROSTIE; PS00076; CHITINBINDNG; 1.

DR PROSTIE; PS00773; CHITINBINDNG; 1.

PROSTIE; PS00774; CHITINBER 19-1; 1.

WHYDROLASS; Glycosidass; Chitin degradation; Chitin-binding; Signal; I.

SIGNAL 1.

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 LRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ATSPPYY 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDI 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
HYDROLASES).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 KREVAAFLAQTSHETTGGWATAPDGPYTWGYCFKEENGGAGPDYCQQSAQWPCAAGKKYY
                                                                                                                                                                                                                       Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                   chitinase.";
Mol. Gen. Genet. 226:289-296(1991).
-!- FUNCTION: THIS PROPEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhu Q., Lamb C.J.; "Isolation ard characterization of a rice gene encoding a basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
BASIC ENDOCHITINASE 2.
CHTIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 336;
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SIMILARITY.
7F4EC126265DEA84 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.9%; Score 747.5; DB 1; 57.3%; Pred. No. 3.8e-55; ive 28; Mismatches 63;
                                                                                                         01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-DC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  336 AA
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=91238706; PubMed=2034221;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MM;
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                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3336
3336
339
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Matches 142; Conserv
                                                                                                                                                                                                         Oryza sativa (Rice)
Eukaryota; Viridipl
                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                                         CHI2_ORYSA
P25765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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                                                     CHI2_ORYSA
                                       RESULT 11
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                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots; Vitaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nuterPro; IPRO0102; Chitin_bind.
InterPro; IPRO0102; Chitin_bind.
InterPro; IPRO0102; Clitin_binding.
Pfam; PF00187; chitin_binding; 1.
Prim; PF00182; Glyco_hydro_19; 1.
Prim; PF000851; CHITINBINDNG.
ProDom; PD000699; CHITINBINDNG.
ProDom; PD000699; Chitin_bind; 1.
SMART; SM00270; ChtBD1; 1.
PROSITE; PS00026; CHITIN_BINDNG; 1.
PROSITE; PS00074; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant Physiol. 115:1029-1038(1997).

-1. FUNCTION: DEPENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.

-1. CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4 BETA-LINKAGES OF

N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO

CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Busam G., Kassemeyer H.H., Matern U.; "Differential expression of chitinases in Vitis vinifera L. responding to systemic acquired resistance activators or fungal challenge.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
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Y SIMILARITY.
Y SIMILARITY.
SY SIMILARITY.
3802484ED69EC6C0 CRC64;
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CHITIN-BINDING (BY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 1.7e-54;
                                                              01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-UL-1999 (Rel. 38, Last annotation update)
15-IUL-1999 (Rel. 38, Last annotation update)
314 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 739.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. PINOT;
MEDLINE=98052138; PubMed=9390436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z54234; CAA90970.1; -.
HSSP; P23951; ZBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%;
48.2%;
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Query Match
Best Local Similarity
Matches 139; Consery
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHI1_GOSHI
Q39799;
                                                                                                                                                                         DISULFID
DISULFID
SEQUENCE
                                                                                                                                     DOMAIN
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHI1_GOSHI
                                                                                                                          CHAIN
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 ~;
                                                                                                                                                                                                      240
                                                                                                                                                                                                                               249
                                                                                           129
                                                                                                                                                  121 AAFLAQTSHETTGGWASAPDGPYAWGYCYLREQGSPGAYCVPSAQWPCAAGRKYYGRGPI 180
                                                                                                                                                                             189
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- CATALYTIC SCITULTY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- INDUCTION: BY FUNGAL INFECTION.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Collinge D.B.;
"Accumulation of defence-related transcripts and cloning of a chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with Ascochyta pisi Lib.";
Plant Sci. 92:69-79(1993).
-! - FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Embryophyta; Tracheophyta;
                                                                                                                                                                             130 QLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWT
                                                                                                                                                                                                                              PTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCY
                                                                                                                                                                                          1 MGLWALVAFCLLSLILVGSAEQCGGQAGGRVCPGGACCSKFGWCGNTADYCGSGCQSQCS
                                                                                                                           --ATSPPYYGRGPI
                                                                          ---GVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Reurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum.
NCBL_TaxID=3888;
 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=CV. BIRTE; TISSUE=Leaf;
Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
   Indels
  78;
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
                           MARFAALAVCAAALLLA~-------VAAGGAAAQ--
                                                                                                                                                                                                                                                                                                                                                                        320 AA
   Mismatches
                                                                                                                              84 AAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum sativum (Garden pea).
Eukaryota, Viridiplantae, Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                       ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       interPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONTAINING FUNGAL PATHOGENS.
   30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X63899; CAA45359.1; -.
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
      Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   250 TQRNFAS 256
                                                                                                                                                                                                                                                                                                             301 NORPEGS 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                          CHIX_PEA
                                                                                                                                                                                                                                                                                                                                                                                       P36907
                                                                                                                                                                                                                                   190
                                                                                                                                                                                                                                                                                                                                                               CHIX_PEA
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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GOSSYPIUM hirsutum (Upland cotton).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyladons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186 RRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGN 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 GRWTPSAADSSAGRVPGYGVITNINGSIECGHGQDNRVDDRVGFYRRYCQIFGVDPGGN 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RGPIQLTGRSNYDLAGRALGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVAL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---ATSPPYYG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            131 KKKELAAFLAQTSHETTGGWPTAPDGPYAWGYCFVSEQNTQEVYCSPKDWPCAPGKKYYG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CV. COKER 201:

STRAIN=CV. COKER 201:

Levorson J.P., Chlann C.A.;

Levorson J.P., Chlann C.A.;

Levorson J.P., Chlann C.A.;

Levorson J.P., Chlann C.A.;

similarity to class I endochitinase plant sequences.";

(In) Plant Gene Register PGRSP6-054.

(In) Plant Gene Register PGRSP6-054.

-!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF

N-ACETYL-D-GIUCOSAMINE POLYMBRS OF CHITIN.

-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO

-IS SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO

CLASS IB IN THE CAPALYTIC PART BUT WHICH INCLUDE A N-TERMINAL

CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 AAGGAAAQGYGSVIIRSVYASMLPNRDNSLCPARGFYIYDAFIAAANTFPGFGIIGSADD 78
                                                                                                                                                                                  Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.1%; Score 723; DB 1; Length 320; 55.6%; Pred. No. 4e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                7EDEC8CLAECC3435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 IKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKBEISK----
                                                                                                                                                                                                                                                                                                  (BY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update
                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                      ENDOCHITINASE. CHITIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                             SIMILARITY
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
SMART; SM00270; Chibbl; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE 19_1; 1.
PROSITE; PS00774; CHITINASE 19_2; 1.
Hydrolase; Glycosidase; Chitin degradat Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33;
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320
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34507 N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 LDCYTQRNFA 255
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the European Bioinformatics and the EMBL outstation use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 AGGAAAQGVG---SVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSA 76
                                                                                                                                                                                       InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00107; chitin_binding; 1.
Pram; PF001082; Glyco_hydro_19.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD0006574; Glyco_hydro_19; 1.
ProDom; PD000699; Chitin_bind; 1.
SMART; SM00270: ChitBD1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_2; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideee; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 PYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVALRRWIPTAADTAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18;
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ENDOCHTINASE 1.
REMOVED IN MATURE FORM (BY SIMILA CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, 9923B123EF5C7E3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53.1%; Score 723; DB 1; Length 324; 53.3%; Pred. No. 4e-53; ive 35; Mismatches 66; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14)
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                                                                                                                                                        EMBL; U60197; AAB67842.1;
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 53.3
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 TGGNLDCYTQRNFAS 256
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SEQUENCE FROM N.A.
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P24626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H HSSP, P02877; 1HEV.

R HSSP, P02877; 1HEV.

R InterPro; IPR001002; Chitin_bind.

R InterPro; IPR001002; Chitin_bind.

R Fam; PF00182; Clyco_hydro_19.

R PRINTS; PR00451; CHITINBINDMG.

R PRODOM; P0000609; Chitin_bind; 1.

R PRODOM; P0000609; Chitin_bind; 1.

R PROSITE; PS00026; CHITIN_BINDMG; 1.

R PROSITE; PS00075; CHITIN_BINDMG; 1.

R PROSITE; PS00773; CHITIN_BINDING; 1.

R PROSITE; PS00774; CHITINASE_19_1; 1.

R Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;

Multigene family.

I POTENTIAL.

SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --ATSPPY 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19 AAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADD 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 ALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTAIG
                                                                              "Nucleotide sequence of a rice genomic clone that encodes a class
  MEDLINE-91370895; PubMed=1893114;
Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
Muthukrishnan S., Reeck G.R.;
                                                                                                                               Plant Mol. Biol. 16:479-480(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                          CONTAINING FUNCAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASIC ENDOCHITINASE 1
CHITIN-BINDING (BY SI
BY SIMILARITY.
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BY SIMILARITY.
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Pred. No. 5.2e-53;
1; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 IKRDLAAFFGQTSHETTGGTRGAAD-QFQWGYCFKEEISK---
JAPONICA; TISSUE-Seedling;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X54367; CAA38249.1; -.
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33695 1
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Matches 141; Conservative
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305 DNLDCYNQRPY 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 GNLDCYTORNF 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AA;
                                                                                                                                                                                                                                                                                                                     HYDROLASES)
                                                                                                            endochitinase.
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Search completed: May 3, 2002, 18:48:31 Job time: 915 sec

us-09-534-229c-1.rsp

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May 3, 2002, 18:32:16; Search time 157.87 Seconds (without alignments) 237.193 Million cell updates/sec
                                                                                                                                                 US-09-534-229C-1
1362
1 MARFAALAVCAAALLLAVAA......MLGTATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                               473505
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                  473505 seqs, 146272329 residues
                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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sp_bacteria:*
sp_lungi:*
sp_lungi:*
sp_lunma:*
sp_invertebrate:*
sp_mammal:*
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sp_phage:*
sp_plant:*
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Maximum DB seq length: 200000000
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55:
77:
10:
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Perfect score:
Seguence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description				oryza	٠.			oryza sa	solanum 1	solanum	solanum.						Q42839 hordeum vul	Q9frv0 secale cere	Q9sxjl arabis gemm
SUMMARIES	QI	043764	Q9AXR8	043765	O9FWE9	080423	O9LEH7	Q9FWE7	004271	043835	6PaseQ	043834	022568	024007	082552	042515	043294	042839	O9FRVO	Q95XJ1
	DB	10	10	10	10	1.0	10	10	10	10	10	10	10	10	10	10	10	10	10	10
	Query Match Length	256	252	252	261	261	249	296	289	236	251	252	240	175	253	264	340	332	266	335
æ	Query Match	97.9	93.8	93.0	83.7	.82.9	82.8	73.4	71.5	9.09	60.4	60.4	60.2	59.8	59.4	59.1	58.6	56.7	56.4	56.3
	Score	1334	1277	1266	1139.5	1128.5	1128	1000	973.5	825.5	822.5	822.5	819.5	814	808.5	50	797.5	772.5	768	767
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09M7G7	Q9FRV1	Q9FPM1	042994	09M7H7	09M7H1	042993	09M7F6	P93680	080404	09M7G4	00000	TD/WAD	Q9M7H2	Q9M7F5	09M7H4	09M7H0	042992	09M7G0	09M7F7	09M7G2	09SX.T4	1 L L L L L L L L L L L L L L L L L L L	ממים מים	095838	Q9M7F4	Q9M7G9	Q9SXJ2
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ALIGNMENTS

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61 IAAANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 PPYYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                 Hordeum vulgare (Barley).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.

NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Oryza sativa (Rice).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales: Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HNVALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MARFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES
ACETYL-OGLOCOSAMINE POLYMERS OF CHITIN.
EMBL; X78672; CARA5345.1;
HSSP; P23951; 2BAA.
                                    01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-NOV-1996 (TEMBLrel. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. PALLAS, NEAR-ISOGENIC LINE PO2: TISSUE-LEAF;
Bryngelsson T., Collinge D.B., Green B., Gummesson P.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8A6209D443E8FDD8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1266; DB 1U;
Pred. No. 4.3e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Mismatches
      252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                       Mendel, 25, Horru;Chiao;25.
InterPro; IPR000726; Glyco,hydro_19.
Priam; PR00182; Glyco_hydro_19; 1.
Propom; Pp000574; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26629 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.0%;
Best Local Similarity 93.0%;
Matches 238; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 ATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGGNIDCYTORNFAS 252
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          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                              Thordal-Christensen H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252 AA;
                                                                                                                             CHIAO OR CHIZE
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01-JUN-2001 (
CHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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          Q43765
Q43765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IAAANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MARFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF 60
                                                                                                                                                                240
                             IAAANTEPGEGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATS 120
                                                  PPYYGRGPIQLIGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSC 180
                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=2053799; Pubmed=11080301;
Yebh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wiseman S.B.
Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in
MARPAALAVCAAALLLAVAVGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAF
                                                                                                                                                                  HNVALRRWIPTAADTAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lajoie G.; "Chitinase genes responsive to cold encode antifreeze proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 252;
                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2001 (TIEMBLIEL 17, Last sequence update)
01-JUN-2001 (TIEMBLIEL 17, Last annotation update)
24.8 KDA CLASS II ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
Secale cereale (Rye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FC9D538F49690823 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.8%; Score 1277; DB 10;
93.8%; Pred. No. 4.9e-102;
iive 7; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                      252 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          winter cereals.";
Plant Physiol. 124:1251-1264(2000).
                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26835 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF280438; AAG53610.1;
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Best Local Similarity 93.89
Matches 240; Conservative
                                                                                                                                                                                                                                                         241 ATGGNLDCYTQRNFAS 256
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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Signal. SIGNAL

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Indels

261 AA.

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RESULT Q9AXR8

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Gaps

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Pred. No. 2.9e-89;
Mismatches 24; Indels
                                      Mismatches
                                      21;
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01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
      82.0%;
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                                         209; Conservative
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             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHITINASE II. CHT2.
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                                                   STRAIN-CV. NIPPONDRRE;
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Burr P.C.,
Hsiao J., Zismann V., Pai G., Bowman C.L., Fujil C.Y., Vanaken S.E.,
Bowman C.L., Cramann T.V.,
Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
Coryza sativa chromosome 10 BAC OSINBb0015111 genomic sequence.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ACO51633, AAG13608.1; -.
InterPro; IPRO00726; Glyco_hydro_19.
Fram, PRO0182; Glyco_hydro_19: 1.
PROSITE; PSO00773; CHITINASE_19_1; 1.
PROSITE; PSO00773; CHITINASE_19_1; 1.
SEQUENCE 261 AA; 27551 MW; 773133E7813DFDBE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVALRRWIPIAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYIRYCGMLGTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 AANTFPGFGTT-GSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSP 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JEMONEAL FACABLE AND ALCANDE AND ALCAND ALCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.7%; Score 1139.5; DB 10; Length 261; 82.7%; Pred. No. 3.2e-90; ive 20; Mismatches 23; Indels 1;
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Last annotation update)
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6760C2578121E0BF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 IGGNIDCYTORNFAS 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 AA;
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Matches 211; Conserv
                                  SEQUENCE FROM N.A.
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8 δă Db ă Length

DB 10;

82.9%; Score 1128.5;

Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDAVVSFRTAMWEMMTAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITNIINGGLEC 216
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                                                                                                                                                                                                                                           182 NVALRRWIPTAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
                                       99
3 RFAALAVÇAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 YASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLAAFFGQTSHETTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Green R.M., Bevan M.; "Isolation of genes induced in barley during powdery mildew infection."; submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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EMBL; AJZ76226; CAB99486.1; -
EMBL; AJZ76226; CAB99486.1; -
Interpro; IPRO00726; Glyco_hydro_19.
Probom; PF00182; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE.19.1; 1.
PROSITE; PS00774; CHITINASE.19.2; 1.
SRQUENCE 249 AA; 27127 MW; ED85AB6E9E6FEB88 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
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93.6%; Pred. No. 3e-89;
Live 8; Mismatches 6;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                       TISSUE=LEAF;
                                                                                                                                                                                                   SEQUENCE OF 32-289 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 74.49
Matches 186; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GNLDCYTORN 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                276 SNLDCYNQRN 285
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                                                                                              SECUENCE FROM N.A.
                                                                                                                                                                                                                          STRAIN-CV. IR36;
                                                   NCBI_TaxID=4530;
                                                                                                                    STRAIN=IR36;
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DR EMBL, ACO51633, AAG135901.; DR EMBL, ACO51633, AAG135901.

DR PRODON: PD000726; Glyco_hydro_19.

PRODON: PD0007574; Glyco_hydro_19; 1.

DR PRODON: PS000773; CHITNASE_19_1; 1.

RFOUTHCE 296 AA; 32169 MW; ICOFR158E5CF119B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         149 VSNPDLVSTDAVVSFRTAMWFWWTAQGNKPSCHNVALRRWTPTAADTAAGRVPGYGVITN 208
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                 150 IDAVYSFRTAIWFWMTAQGNKPSSHDVALGRWTPTAADTAAGRVPGYGVITNLINGGLEC 209
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AANTEPGEGIT-GSADDIKRDLAAFEGQISHETIGGIRGAADQFQWGYCFKEEISKAISP
                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae,
Ehrhartoideae; Oryzeae; Oryza.
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Last annotation update)
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Last annotation update)
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ilarity 67.7%; Pred. No. 3.6e-78;
Conservative 22; Mismatches 33;
                                                            289 AA
                                                                                                                                                                                                                 296 AA.
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08,
17,
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Best Local Similarity
Matches 195; Conserv
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01-NOV-1998
01-JUN-2001
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65 NIFPGFGTIGSA-DDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSFPY 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chitinase in
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots;

Aspermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 ALRRWIPTAADIAAGRVPGYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGIAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ż
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 VCAA----ALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant Mol. Biol. 35:749-761(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CLASS II CHITIARSE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-FACETYLGLUCOSAMINIDASE) (FRAGMENT).
CHIAO OR CHTAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71.5%; Score 973.5; DB 10; Length 289; 74.4%; Pred. No. 6.6e-76; Live 19; Mismatches 38; Indels 7;
                                                                                                                                                                                                                                    Comparative, 1 and 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              remainer K., Stromberg A., Schmelzer E., Kombrink E.; "Frimary structure and expression of acidic (class.II) potato.";
run C.-H., Lee B.P., Yun K.J., Eun M.Y.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-CV DATURA; TISSUE-LEAF;
MEDLINE-98088002; Pubmed-9426596;
Buchter R., Stromberg A., Schmelzer E., Kombrink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         236 AA.
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NON_TER SEQUENCE

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--GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 AFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQIJGRSNYDLAGRAI 144
                                                                                                       145 --GKDLVSNPDLVSTDAVVSFRIAMWFWMIAQGNKPSCHNVALRRWIPIAADIAAGRVPG 202
                                                                                                                                  01-NOV-1996 (TEMBLRel. 01, Last sequence update)
01-JUN-2001 (TEMBLRel. 17, Last annotation update)
CLASS II CHITINASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 AQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AQNAGSIVTRELEEQMLSFRNDVCPGKGFYTYDAFIAAANSFPAFGTTGDDTARKKEMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridin lantae; Streptophyta; Embryophyta; Tracheophyta; Sparmatophyta; Varidin landiophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                        22 AQNAGSIVTRELFEQMLSFRNNDVCPGKGFYTYDAFIAAANSFPAFGTTGDDTARKKEMA
                                  85 AFFGQISHETTGGIRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAGRAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Mol. Biol. 35:749-761(1997).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
EMBL; U49969; AAB96341.1; -.
                                                                                                                                                                                                  203 YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27491 NW; 2DC63CEB2C319B31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. DATURA; TISSUR-LEAF;
MEDLINE-98088002; PubMed-9426596;
Buchter R., Stromberg A., Schmelzer E., Kombrink E.
"Primary structure and expression of acidic (class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60.4%; Score 822.5; DB 1
65.7%; Pred. No. 5.2e-63;
iive 28; Mismatches 45,
                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                              252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P23951; 2BAA.

Mendel; 14796; Soltu;ChiaO;14796.

InterPro; IPR000726; Glyco_hydro_19.

Pfam; PF00182; Glyco_hydro_19. 1.

ProDom; P000054; Glyco_hydro_19; 1.

PROSITE; PS00773; CHITINASE_19_1; 1.

PROSITE; PS00774; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                  Q43834 PRELIMINARY; PRT;
Q43834;
01-NOV-1996 (TrEMBLRel. 01, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                             CHIAO OR CHTA2.
Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 65.7
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Glycosidase.
SEQUENCE 252 AA; 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            145
                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                   Q43834
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                                                                                                                                                                                                                                                                                                                                                                                                                AFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAGRAL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                     --GKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPG 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                          84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum (Potato).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                        25 AQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA
                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 YGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10; Length 236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primary structure of potato acidid (class II) chitinase.";
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
EMBL: AF024537; AAB81962.1; -.
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60.4%; Score 822.5; DB 10; Length
65.7%; Pred. No. 5.1e-63;
Live 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 AA; 27359 MW; B4C63CF915319BlA CRC64;
                                                                                                                                                                                                                 216C86B55D8CC7FB CRC64)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TIEMBLIEL. 13, Created)
01-MAY-2000 (TIEMBLIEL. 13, Last sequence update)
01-JUN-2001 (TIEMBLIEL. 17, Last annotation update)
CLASS II CHITINASE (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=CV. DATURA; TISSUE=ELICITOR-TREATED LEAVES; Kombrink E.;
                                                                                                                                                                                                                                                                                                            44;
                                                                                                                                                                                                                                                                    60.6%; Score 825.5; DB 1
65.7%; Pred. No. 2.6e-63;
cive 29; Mismatches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           251 AA
                    CHITIN.
                              EMBL: U49970; AAB96340.1:
HSSP; P23951; 2BAA.
Mendel: 14797; Soltu:Chia0:14797.
InterPro: 19R000726; Glyco_hydro_19.
Pfam; PF00182; Glyco_hydro_19; 1.
PROSITE; PS00773; GHTINASE_19_1:
PROSITE; PS00774; CHTINASE_19_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF00182; Glyco_hydro_19; 1.
Probom: PD000574; Glyco_hydro_19; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P23951; 2BAA.
InterPro; IPR000726; Glyco_hydro_19.
                    Ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                    ACETYL-D-GLUCOSAMINE POLYMERS
                                                                                                                                                                                                                     236 AA; 25723 MW;
                                                                                                                                                                                                                                                                            Query Match 60.6%,
Best Local Similarity 65.7%,
Matches 153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                153; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycosidase.
NON_TER 1 1
                                                                                                                                                                               Hydrolase, Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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09SBJ9

II) chitinase in

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Gaps

7;

45;

DB 10; Length Indels

RESULT 10
098819
AC 098819
AC 098819
DT 01-MAX
DX NONLT
DX EMBL;
DX EMBL;
DX EMBL;
DX EMBL;
DX HOSP;
DX PROSII

197

25 AQGVGSVIIRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA 84

Best Local

Matches

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.; 0

Gaps

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9

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(1)

RA

RA

HWANG B.K., HONG J.K., Kim Y.J.;

RA

"Molecular cloning and characterization of a pathogen-induced gene

RT

"Molecular cloning and characterization of a pathogen-induced gene

RT

Submitted (SEP-1998) to the BMBL/GenBank/DDBJ databases.

BR SA091235; AAC36359.1;

DR HSSP; R23951: 2BAA.

Mendel; 33139; Capan;Chia0;33139.

DR HOREPTO: IPR000726; Glyco_hydro_19.

DR ProDom; PD00574; Glyco_hydro_19.

DR PROSITE; PS00773; CHITINASE_19_1.

DR PROSITE; PS00774; CHITINASE_19_2; 1.

DR PROSITE; PS00774; CHITINASE_19_2; 1.

DR PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 ANTFPGFGTTGSADDIKRDLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPY 123
                                                                                                                                                                                                                                                                                                                              82 DLAAFFGQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAG 141
                                                                                                                                                                                                                                                                                                               142 RAIGKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capsicum annuum (Bell pepper).

Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.

NCBI_TaxID=4072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 FAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAA
                                                                                                                                                                                                                                                                            202 GYGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTAIGGNLDCYTQRNPAS 256
                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 253;
                                                                                                                                                                                                        Length 175;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                  175 AA; 18969 MW; 48933B1BAFCB1FCE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                        ; Score 814; DB 10;
; Pred. No. 1.8e-62;
13; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59.4%; Score 808.5; DB 1
59.4%; Pred. No. 8.3e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                             59.8%;
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08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 59.4
Matches 151; Conservative
                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 01-NOV-1998 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                                                                                                                             Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHITINASE CLASS II.
                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHIAO OR CACHIZ.
                                                                                                                                                                                                                                           Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                 Query Match
                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
082552
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85 AFFCQTSHETTGGTRGAADQFQWGYCFKEEISKATSPPYYGRGPIQLTGRSNYDLAGRAI 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kim C.Y., Gal S.W., Choe M.S., Jeong S.Y., Lee S.I., Cheong Y.H., Lee S.H., Choi Y.J., Han C.D., Kang K.Y., Cho M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GKDLVSNPDLVSTDAVVSFRTAMWFWMTAQGNKPSCHNVALRRWTPTAADTAAGRVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIAAANTFPGFGTTGSADDIKRDLA
                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         203 YGVIINIINGGLECGMGRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                      240;
                                                                                                                                                          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum. NCBI_raxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                          Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF024538; AAB81963.1; --
HSSP; P23951; ZBAB.
HSSP; P23951; ZBAB.
HSSP; P23951; SOLtu; ChiaO; 27051.
InterPro; JRF000726; Glyco_hydro_19.
ProDom; PD000726; Glyco_hydro_19; 1.
PROSITE; PS00073; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                             26258 MW; 0B41665702B11709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JAN-1998 (IrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (FRAGMENT).
                                                                                   01-JAN-1998 (TrEMBLrel. 05, Last sequence update) 01-JGN-2001 (TrEMBLrel. 17, Last annotation update) CLASS II CHITINASE (EC 3.2.1.14) (FRAGMENT). CHIAO OR CHTAA.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-CV. DATURA; TISSUE-ELICITOR-TREATED LEAVES;
Kombrink E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   60.2%; Score 819.5; DB 10;
65.2%; Pred. No. 8.8e-63;
iive 30; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ā
                                             AA.
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                                             240
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                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=LEAF;
MEDLINE=98278381; PubMed=9517819;
                                             PRT;
                                                                         (TrEMBLrel. 05,
                                                                                                                                            Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase, Glycosidase.
NON_TER 1 1
SEQUENCE 240 AA; 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4530;
                                                                         01-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152;
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                                                022568
                                                               022568
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                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. NC 4;

MEDLINE=96178874; PubMed=8616259;

MEDLINE=96178874; PubMed=8616259;

Rellmann J.W., Kleinow T., Engelhardt K., Philipp C., Wegener D.,

Schell J., Schreier P.H.;

Characterization of two class II chitinase genes from peanut and

"Characterization of two class II chitinase genes from peanut and

"Characterization of two class II chitinase genes from peanut and

"Characterication of two class II chitinase genes from peanut and

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arachis hypogaea (Peanut).
Eukaryota: Viridiplantae: Streptophyta: Embryophyta; Tracheophyta; Spermatophyta: Magnoliophyta; edicotyledons; core eudicots; Rosidae; eurosids I: Fabales; Fabaceae; Papilionoideae; Arachis.
NCBI_TaxID=3818;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RFAALAVCAAALLLAVAAGGAAAQGVGSVITRSVYASMLPNRDNSLCPARGFYTYDAFIA 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVALRRWIPTAADIAAGRVPGYGVITNIINGGLECGMGRNDANVDRIGYYTRYCGMLGTA 241
                                                                                                                                                                                                                     124 YGRGPIQLTGRSNYDLAGRAI--GKDLVSNPDLVSTDAVVSFRTAMMFWMTAQGNKPSCH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       116 SKATSPP-----YYGRGPIQLTGRSNYDLAGRAIGKDLVSNPDLVSTDAVVSFRTAMWF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 805.5; DB 10; Length 264;
; Pred. No. 1.6e-61;
35; Mismatches 63; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLREL. 17, Last annotation update)
CHITINASE (EC 3.2.1.14) (CHITODEXTRINSE) (1,4 "BETA-POLY-N-ACETYLGJUGOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
CHIA2 OR CHI2,2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Glycosidase.
SEQUENCE 264 AA; 28924 MW; CCB13C590ADB5D8A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                264 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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Best Local Similarity 57.4%;
Matches 152; Conservative 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                            242 TGGNLDCYTQRNFA 255
                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q42515
Q42515;
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230 YYTRYCGMLGTATGGNLDCYTQRNF
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             qq
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3, 2002, 18:46:59 Search completed: May Job time: 883 sec

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May 3, 2002, 18:30:29; Search time 117.39 Seconds (without alignments) 203.814 Million cell updates/sec
                                                                                                                                                                                                                                                 US-09-534-229C-2
1792
1 MSTLRARCATAVLAVVLAAA......YGNNLDCYNQLSFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDSZ/gcgdatz/geneseq/geneseqp/AA1980.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1981.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1981.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1983.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1983.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1985.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1986.DAT:*
/SIDSZ/gcgdatz/geneseq/geneseqp/AA1986.DAT:*
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/SIDS2/gcgdatu/geneseq/geneseqp/AA1990 DAT:*
/SIDS2/gcgdatu/geneseq/geneseqp/AA1991 DAT:*
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/SIDS2/gcgdatu/geneseq/geneseqp/AA1992 DAT:*
/SIDS2/gcgdatu/geneseq/geneseqp/AA1994 DAT:*
/SIDS2/gcgdatu/geneseq/geneseqp/AA1995 DAT:*
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Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                        522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 200000000
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Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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Maximum DB s
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                                                                                                       OM protein
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                                                                                                                                                      Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

6 1230 6 7 1230 6 8 1177.5 6 9 1177.5 6 1 177.5	68.6 68.6 65.7 7.7	336 136 336 136 336 22 324 12 324 12 324 12	AANYSUGU AAR29019 AAR67969 AAR13275 AAR31297 AAR31297	RCH10 chitinase pr Rice chitinase. O Amino acid sequenc Tobacco intracellu Nicotiana sp. intr
	65.3	329 12	AAR15841	Basic chitinase 48

Chitinase. Cucurb	O)	e]	ē	S(e)	Ø	Chitinase G. Hord	Floral organ-speci	anana ripeni	formis ch			Petunia hybrida ex	Amino acid sequenc	O	Wheat chitinase pr	Sugar beet chitina	Rye chitinase-like	Rye chitinase-like	Wild tomato endoch	A maize chitinase	Wild tomato endoch		Arabidopsis thalia	Arabidopsis thalia	Protein encoded by	cid	A maize chitinase		gar beet chit		Sugar beet chitina	g	A maize chitinase
AAW2455		AAW00	AAR20822	AAR56	AAR20820	AAR5257	AAW647	AAY0584	AAW9016		AAR1327	AAW3129	AAB075						AAR76713				AAG28415	AAG2841	AAB2878	AAB1890	AAB1890	AAB1893	AAR2814	AAB1889		AAG5365	AAB1889
18	12	17	13	15	13	15	19	20	20	21	12	18	21	16	22	13	20	20	16	21	16	21	21	21	22	21	21	21	13	21	13	21	21
292	331	317	328	329	303	266	328	2466	243	259	254	254	254	253	256	439	252	230	250	252	253	284	272	280	372	155	271	271	268	281	264	813	328
64	64	64	63	63	9	58	58.7	53	49	46	45	45	45	45	44	44	44.	43.	43	43.	43.	43.	43.	43.	39.	36.	35.	35.	33.	33.	32.	27.	26.
1163.5	i .	1160	\vec{a}	1141.5	Ö		1052.5		879	827		818.5		809	798	795	790	786	779.5	779.5	775.5	774	770.5	770.5	707.5	644.5	633	633	597.5	595.5	584	492	480.5
12	13	14	15	9	17	. 60	19	20	21	22	23	24	25	26	27	28	29	30	31	32	i m	34	35	36	37	38	5 6	40	41	42	43	44	45

ALIGNMENTS

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This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression
                                                                                                                                                                                                                                                                                                                           New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes .
                                                                                                         Wheat; chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; rye.
                                                                                   Wheat chitinase protein homologous to rye chitinase.
                                                                                                                                                                                                                                                                             (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
          AAB11488 standard; protein; 323 AA.
                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Fig 2; 11pp; Japanese.
                                                                                                                                                                                                                           99JP-0081694
                                                                                                                                                                                                                                                    99JP-0081694
                                                              (first entry)
                                                                                                                                                                                                                                                                                                     WPI; 2001-027417/04.
                                                                                                                                                  Triticum aestivum.
                                                                                                                                                                           JP2000270866-A.
                                                                                                                                                                                                                            25-MAR-1999;
                                                            02-MAR-2001
                                                                                                                                                                                                                                                     25-MAR-1999;
                                                                                                                                                                                                   03-OCT-2000.
                                   AAB11488;
AAB11488
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245
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                                                                                                                                                                                                                                                         243
                                                                                                                                                                                                                                                                                                                                               RESULT
AAW98079
ID AAW98
XX
                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                   qq
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                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                        g
                                                                                                                                                                                              g
                                                                                                                                                                                                                  δλ
                                                                                                                                                                                                                                                         QΥ
  SS \times S
                                                                                                 δy
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                                                                                                                                      δ
                                                                                                                                                                            Qγ
                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat PII/3438 (of high snow mould resistance). The genes are
chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat PII73438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant pathogenic microbes.
                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                SCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIF 300
                                                                                                                                                          61 RCQSQCTGCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
                                                                                                                                                                                                TGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCA 180
                                                                                                                                Gaps
                                                                                                                    09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \boldsymbol{w} temperature expression chitinase gene for producing a plant highly resistant to psychophilic plant pathogenic microbes \phantom{x} .
                                                                                                                    1 MSTLRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP
                                                                                                                                                                                                                                      PGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheat, chitinase; low temperature expression; hardened; plant; snow mould resistance; psychophilic plant pathogen; spring wheat.
                                                                                                  0;
                                                                               Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Wheat chitinase protein homologous to spring wheat chitinase.
                                                                                                  Indels
                                                                               DB 22;
                                                                             Query Match 100.0%; Score 1792; DB 22; Best Local Similarity 100.0%; Pred. No. 2.6e-144; Matches 323; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HOKK-) HOKKAIDO NOGYO SHIKENBACHO.
                                                                                                                                                                                                                                                                                                                                                                                        AAB11489 standard; protein; 319 AA
                                                                                                                                                                                                                                                                                                                               301 GIGYGNNLDCYNQLSFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 7; Fig 3; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99JP-0081694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99JP-0081694
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-027417/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum
                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JP2000270866-A.
                                                     323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                           AAB11489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      low
                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 grade
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                                                                                                                                                                                                                                                                                                                                                                   RESULT
AAB11489
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     8X66666
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1;
useful for creating a plant grade, highly resistant to psychophilic plant
pathogenic microbes.
                                                                                                                                                                                                                                                                                                                                                                                                                                             HDVITGLWIPTARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGI 302
                                                                                                                                                                                                                                                                                                        KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 G------GGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTIG 122
                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                       64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye, antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy.
                                                                                                                                                                     12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG
                                                                                                                                                                                              "mature protein, also claimed in Claim 10"
                                                                                                      Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding antifreeze polypeptides from plants
                                                                                                                                        Indels
                                                                                                      DB 22;
                                                                                                                                        48;
                                                                                                    Query Match 72.2%; Score 1294.5; DB 2; Best Local Similarity 71.0%; Pred. No. 4.5e-102; Matches 223; Conservative 34; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rye chitinase-like protein CHT9 preprotein.
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1..20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moffatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-CA00745.
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/note= "r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 GYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||:||||||| |
305 sygdmldcyngrpf 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Griffith M, Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-153795/13.
                                                         AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secale cereale.
                                                         319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9906565-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-JUL-1998;
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                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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Secale cereale.

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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CHT9 preprotein. The mature protein, which is also claimed, is a
chitiasse-like protein that has chitiasse (antifungal) and
antifreeze activities. CHT9 cDNA (see AAXX4889) was obtained by
isolating mRNA from rye plants grown at low temperatures in the
sheence of pathogens or other stresses, i.e. under conditions when
con partial and yeast (First) have been cloned and expressed in
chartinase-like antifreeze activity would be expressed in
The chitinase-like antifreeze proteins can be used: to increase
freezing tolerance of plants and microorganisms; to increase freed
creating tolerance of plants and microorganisms stood to sub-zero
temperatures; to inhibit ice recrystallisation in biological
materials or foods; for cryopreservation and hypothermic protection
of cells, embryos, tissues etc. (particularly human platelets); and
cot cells, embryos, tissues etc. (particularly human platelets); and
progression of diseases or spoilage caused by low temperature
cryopreserved biological material. The signal peptide can be used
cryopreserved biological material. The signal peptide can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------GGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCH 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 dvitgrwspsgadqaagrvpgygvitniingglecgrgqdarvadrigfykrycdllgvs 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy.
particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 LDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 vvvamlaaafavsahaeqcgsqaggatcpnclccskfgfcgstseycgdgcqsqcnrcgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72.0%; Score 1290; DB 20; 71.2%; Pred. No. 1.1e-101; ive 34; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW98080 standard; Protein; 298 AA.
                                                                               Claim 10; Fig 21a; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rye chitinase-like protein CHT9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                         and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             304 YGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 ygdnidcyngrpf 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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       qq
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)

CHT9 mature protein. It lacks the 20-amino acid signal peptide

CC of the preprotein (see AAM98079), which is also claimed. Mature CHT9

is a chitinase-like protein that has chitinase (antifungal) and

continuase-like protein that has chitinase (antifungal) and

contained by isolating mRNA from rye plants grown at low temperatures

contained by isolating mRNA from rye plants grown at low temperatures

contained by isolating mRNA from rye plants grown at low temperatures

contained by isolating mRNA from rye plants grown at low temperatures

contained by isolating mRNA from rye plants grown at low temperatures

continuated and contained contained and confidence of pathogens or cloim and ryes and microorganisms in a ratio for survival of plants, animals and microorganisms exposed to sub-zero

contensatures; to inhibit ice recrystallisation in biological

contained the more colls. They are also used to inhibit initiation and

contained theyos, tissues etc. (particularly human platelets); and

contained the more caused by low temperature

controller in materials or stocker materials.

controller funding material.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 GPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAA 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80 VSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTS 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 HETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNY 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 hettggwptapdgpyswgycfngergapsdycspssgwpcapgkkyfgrgpigisynyy 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 EQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG------GGGGVASI 79
                                                                                                                                                                                                                                                                                                  New nucleic acid encoding antifreeze polypeptides from plants - particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells etcand for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             260 GRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.6%; Score 1265; DB 20; 72.7%; Pred. No. 1.3e-99;
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                                                                                                                                                                                                                      Xiong F;
                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Fig 21d; 118pp; English.
                                                                                                                                                                                                                      Moffatt B,
                                                                                                                 98WO-CA00745.
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                                                                                                                                                                                    (ICEB-) ICE BIOTECH INC
                                                                                                                                                                                                                                                         WPI; 1999-153795/13.
N-PSDB; AAX24889.
                                                                                                                                                                                                                        Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
                                                W09906565-A2
                                                                                                                   31-JUL-1998;
                                                                                                                                                     31-JUL-1997;
                                                                                                                                                                                                                        Griffith M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  216;
                                                                                   11-FEB-1999
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ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMT
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298 rycdilgvsyganldcysg
                                                                                                                                                                                                                                                                                   Thanatephorus cucumeris.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1995-067090/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAQ81346
                                                                                                                                                                                                                                Rice chitinase.
                                                                                                                                                                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                          16-JUL-1993;
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Matches
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    175
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                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence given is encoded by the rice chitinase gene. The promoter region of this gene (see AAQ11407) is responsive to physical and/or biological stress. The pattern of expression of this protein in mature plants is characteristic. There is a low level of expression in autre laves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQCT-----GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PARGITGDLDTRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ 63
                                                                                                                                                                           Location/Qualifiers
123..323
/note= "Region conserved between class I and class
II chitinases"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is
                                                                                                            Promoter; region; rice; chitinase; physical; biological; stress; leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes.
                                                                                                                                                                                                                                                                                                                                                                                          DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1230; DB 13
Pred. No. 1.4e-96;
1; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 33-34; 45pp; English.
                                                                                                                                                                                                                                                                                                                     (SALK ) SALK INST BIOLOGICAL STUDIES.
                            Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
                           standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.68;
69.38;
                                                                                                                                                                                                                                                                           92WO-US04282.
                                                                                                                                                                                                                                                                                               91US-0704288
                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                          chitinase protein.
                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-415785/50.
N-PSDB; AAQ31407.
                                                                                                                                                                                                                                                                                                                                                                                                                             expression in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336 AA;
                                                                                                                                                                                                                                                                                                                                         zhu Q;
                                                                                                                                                         Oryza sativa
                                                                                                                                                                                                                                                                          21-MAY-1992;
                                                                                                                                                                                                                                                                                               22-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Simi
Matches 221;
                                                                    20-APR-1993
                                                                                                                                                                                                                                 WO9220807-A
                                                                                                                                                                                                                                                       26-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                           AAR29019
                                                AAR29019;
                                                                                                                                                                                                                                                                                                                                         Lamb CJ,
                                                                                                                                                                             Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118
                  AAR29019
       RESULT
                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \Omega
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δ
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and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 pqspkpscnavatgqwtpsaddqragrvpgygvitniingglecghgeddriadrigfgk 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 LEARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Sphi fragment of rice chitinase RCH10 gene (given in AA081346) an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and
TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase; transgenic plant; disease resistance;
crop improvement; tobacco; Nicotiana tabacum; plant defense;
fungus pathogen; Cercospora nicotinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.6%; Score 1230; DB 16;
69.3%; Pred. No. 1.4e-96;
ive 31; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thanatephorus cucumeris fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 31-32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                           AAR67969 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  grown in crops as a food source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Maher EA,
                                                                                                                                                                            295 RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US07815.
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LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ
                                                                                                                                                                                                                                                                                                                                                                                                                 AAR13275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UXLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fungal
                                                                                                                                                                            175
                                                                                                                                                                                                       178
                                                                                                                                                                                                                                   235
                                                                                                                                                                                                                                                                                                                    298
                                                                                                                                                                                                                                                                                                                                                                          AAR13275
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                                                                                                                                                                                                                                                                                        QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Brill protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomonas spp.. The plant receptors containing heterologous domains are useful for modulating plant receptors to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to
                                                                                                                                                                                                                                                                                                                                                                           Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
                                                                                                            294
                                                                                                                           234
PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS
                                                                                                            235 IQSNKPSCHDVITGLWTPIARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
                                                                  175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTALWFWMT
                                                                                                                                                                                                                                                                                                                                                 sequence of a rice chitinase designated RCH10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             confer desired traits on essentially any plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 45-46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
(SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamb C,
                                                                                                                                                                                                                                                                   AAB67444 standard; Protein; 336 AA
                                                                                                                                                                                   |||||| |: || |||||:|
rycdilgvsyganldcysq 316
                                                                                                                                                                     RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000WO-US20714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0363313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chory J,
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-159858/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ronald P, He Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF54983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         336
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200109283-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1999;
                                                                                                                                                                                                                                                                                                                          15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                     Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                              AAB67444;
                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sp
                                                                                                                                                                     295
                                                                                                                                                                                               298
     116
                               118
                                                                                                                                                                                                                                          RESULT
AAB67444
                                                                                                                                                                                                                                                                                 g
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SQCT------GCGGGGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFLAAAGAF 115
                                   TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYR 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence from which this amino acid was deduced was isolated from a N.tabacum cDNA library following screening with a partial tobacco intracellular chitinase clone. The protein sequence appears twice in the specification but in one (not the one given in this
57
                                                                                                                                116 PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS
                                                                                                                   ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
1 mralavvamvarpflaaav---haeqcgsqaggavcpnclccsqfgwcgstsdycgagcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plants with improved resistance to pathogenic fungi - contains chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roekel JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1..23
/label= signal peptide
2..324
/label= intracellular chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EJ,
CP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meulenhoff
Woloshuk
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                        AAR13275 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                     resistance; phytopathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Melchers LS, 1, Vloemans AA,
                                                                                                                                                                                                                                                                                                                                                                             Tobacco intracellular chitinase.
                                                                                                                                                                                                                                    295 RYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIJKSUNIV TE LEIDEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91EP-0200191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90NL-0000222
                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana tabacum Samsun NN
                                                                                                                                                                                                                                                                                                                                                        14-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MOGE-) MOGEN INT NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-232019/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sela-Buurlage MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ12898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP440304-A.
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3;

Gaps

12;

Length 336; Indels

68.6%; Score 1230; DB 22; 69.3%; Pred. No. 1.4e-96; tive 31; Mismatches 55;

Query Match 68.68 Best Local Similarity 69.38 Matches 221; Conservative

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WPI; 1997-479536/44.
N-PSDB; AAT89952.
                                                                                                                                                                                     Local Similarity
hes 203; Conserv
                                                                                                                                                      324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUL-2000.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB07513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                        Sequence
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                 29
                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                    185 YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244
                                                                                                                                                                                                                                           245 VITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGY 304
                                                                                                                                                                                     64 pggptppgggdlgslisssmfdqmlkhrndnacqgkgfysynafinaarsfpgfgtsgdt 123
                                                                                                                                                                          125 DTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ 184
                                                                                                                                         67 TG--CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                                                         63
                                                                                          Gaps
      file), the Leu codons at positions -23, -21, -15, -12, -11, -8, -7, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266, 274, 286 are translated as Ile.

See AA012897-Q12900.
                                                                                                                                                                                                                                                                                                                                                                                                        antifungal; transgenic plant; synergism; tobacco.
                                                                                                                  CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                         DB 12; Length 324;
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                                                                       ; Score 1177.5; DB 12; Lengt
; Pred. No. 3.9e-92;
45; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cornelissen BJC, Linthorst HJM, Melcher
ff EJS, Sela-buurlage MB, Van ROEKEL JSC;
AA, Woloshuk CP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "intracellular protein"
                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana sp. intracellular chitinase protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1..23
/label= signal_peptide
24..324
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                           AAW31297 standard; Protein; 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0047413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91US-0647B31
                                                                           65.7%;
64.2%;
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                            Intracellular chitinase;
beta-1,3-glucanase gene;
                                                                                                                                                                                                                                                                                 305 GNNLDCYNQLSFNVGL 320
                                                                                            Conservative
                                                                                                                                                                                                                                                                                           |:|||| || || || || || 304 gdnldcgnqrsfgngl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MOGE-) MOGEN INT NV
                                                                            Query Match
Best Local Similarity
                                                    324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vloemans AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Nicotiana sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USS670706-A.
                                                                                                                                                                                                                                                                                                                                                                            11-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bol JF, Co
Meulenhoff
                                                                                              203;
                                                                                                                                                                                                                                                                                                                                                             AAW31297
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                     Sequence
                                                                                                                                                                                                                                                                                                                            6
                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                             RESULT
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                                                                                                                                                                                                                                                                 qq
                                                                                                                                                                                                                                                                                   δ
                                                                                                                             a
                                                                                                                                               δλ
                                                                                                                                                               QQ
                                                                                                                                                                               QΥ
                                                                                                                                                                                               QQ
                                                                                                                                                                                                                QΫ́
            88888%8
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                                                                                                            This sequence represents an intracellular chitinase which is used to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes exhibit a synergistic antifungal effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   245 VITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DIRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TG--CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8 CATAVLAVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                                                       an intracellular chitinase which is used
                                                                                                                                                                                                                                                                                                                                                                                                              Length 324;
Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of an extracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                    Score 1177.5; DB 18;
Pred. No. 3.9e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..23
/note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB07513 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                     Example 4; Fig 2; 42pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     65.78; 64.28; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |:|||| || || || 304 gdnldcgnqrsfgngl 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          305 GNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Nicotiana tabacum L. c.v. Havana 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     셤
 QC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δŽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δy
                                                                                                                                                                                                                                                                                                                                               2;
                                                                                                                                                                                                           The present sequence represents an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1, 3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungi. The recombinant polynucleotides and the process are useful for producing fungal resistant plants.
                                                                                                                                              New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245 VITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGY 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244
                                                                                                                                                                                                                                                                                                                                                                                                           67 TG--CGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                     184
                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                   8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC 66
                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                    Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
oshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ckftalssllfsllllsasaeqcgsqaggarcasglccskfgwcgntndycgpgncqsqc
                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 DTRKREVAAFFGOTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical; hormones; expression; secretion; extracellular
                                                                                                                                                                                                                                                                                                                            DB 21; Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vacuole; targetting; chitinase; glucanase; signal; resistance;
                                                                                                                                                                                                                                                                                                                                                65; Indels
                                                                                                                                                                                                                                                                                                                            65.7%; Score 1177.5; DB:
64.2%; Pred. No. 3.9e-92;
live 45; Mismatches 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Basic chitinase 48 from clone lambdaCHN17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ä.
                                                                                                                                                                                          Example 4; Fig 2A-B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR15841 standard; Protein; 329
                         93US-0047413.
91US-0647831.
     97US-0801563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 GNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1:|||| || || || || 304 gdnldcgnqrsfgngl 319
                                                                                                Woloshuk CP,
                                                                                                                                                                                                                                                                                                                                       al Similarity 64.2
203; Conservative
                                                        RIJKSUNIV LEIDEN
                                                                  MOGEN INT NV
                                                                                                                      2000-498214/44.
                                                                                                                                                                                                                                                                                                324 AA
                                                                                                                               N-PSDB; AAA58910
                                                                                       Cornelissen BJC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-MAR-1992
                                                                                                  Vloemans AA,
                          19-APR-1993;
29-JAN-1991;
      18-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR15841;
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                               Query Match
                                                        (UYLE-)
                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                          Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR15841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δŽ
       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TIGDLDTRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APGKQYYGRGPIQLTHNYNYGPAGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 TG-----CGGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 pggptptpptppgggdlgsiisssmfdqmlkhrndnacggkgfysynafinaarsfpgfg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Attachment of the signal peptide ensures occlusion of expressed prod. in the vacuole while elimination of the signal peptide from a sequence normally contg. it ensures that the expressed product is secreted into the extracellular space, rather than retained in the vacuole. Recombinant DNA may contain a structural gene which protects the plant, e.g. resistance to pathogens, herbicides, insecticides, blocides, environmental stress, etc.; leads to increased produ. of proteins, carbohydrates, etc.; leads to pharmaceuticals such as hormones or immunommodulators. See also AAQ15146-50 and AAQ15330-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
&
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence encoding vacuole targetting peptide - esp. signal region of tobacco chitinase or glucanase gene, and derived recombinant DNA, vectors, etc. functional in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65.3%; Score 1170; DB 12; Length 329;
63.2%; Pred. No. 1.7e-91;
iive 44; Mismatches 66; Indels 8
                                                                                                                                                    318..329
/label= sig_peptide
/note= "used as vacuole targetting peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 64-68; 81pp; English.
Location/Qualifiers
                                              exon1_prod
                                                                                          /label= exon2-prod.
                                                                                                                                   exon3_prod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ryals
                                                                                                                                                                                                                                                                                                                                   91EP-0810430
                                                                                                                                                                                                                                                                                                                                                                           90CH-0002007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203; Conservative
                                                                                                          200..329
/label= es
                                              /label= e
149..199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Boller T, Nauhaus JM,
                                                                                                                                                                                                                                                                                                                                                                                                                           (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-371028/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAQ15147
                                                                                                                                                                                                                                                                                                                                   06-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1990;
                                                                                                                                                                                                                                                  EP462065-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                          Peptide
         Key
Region
                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244
                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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3

300 FGIGYGNNLDCYNQLSFNVGL 320

g

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GYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                       (CIBA ) CIBA GEIGY AG
                                                                                                                                                                                                                                                                                                                                                                                                                       Shinshi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-088356/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 204; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         See also AAQ11094
                                                                                                                                                                                                                                                Nicotiana tabacum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ11093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             level
                                                                                                                                                                                                                                                                                                                                   10-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                              13-SEP-1989;
                                                                                                                                                             30-MAY-1991
                                                                                                                                                                                                                                                                                                        27-MAR-1991
                                                                                                                                                                                                                                                                           EP418695-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a high
                                                                                                                                                                                                                                                                                                                                                                                                                     Meins F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                AAR11305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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       264
                                                                            SESULT.
                                                                                                                               Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ω
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                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fund; plants have this enzyme to protect themselves from pathogenic fund; Thus this enzyme can be used to prevent plants from being infected with pathogenic fungi, and the chitinase gene can be fundi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase and serves for prants combination technology works for various host cells and serves for plant immunity to confer disease resistance on plants as the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                       Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAG 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFERFLIHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHETT 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 eqcgrqangalcpnrlccsqfgwcgntdeycknncqsqctppstgggggggggsvgsinea 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 EQCGSQAGGAKCADCLCCSQFGFCGTTSDXCGPRCQSQC----TGCGGGGGGVASIVSRD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGRVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18; Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitinase derived from pumpkin - used to protect plants against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64.9%; Score 1163.5; DB 18; Lengt
69.6%; Pred. No. 5.3e-91;
.ive 30; Mismatches 54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            ZH SEKIYU SANGYO KASSEIKA CENTER
                                                                                           AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 2; 36pp; Japanese.
                                                                                           AAW24554 standard; Protein; 292
       95JP-0347367.
                                                                                                                                                                                                                                                                                                                                                                 95JP-0347367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAT79940, AAT79941.
                                                                                                                                                                                                                                                                                                                                                                                               ENERGY CORP.
                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1997-380170/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 204; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogenic fungi
                                                                                                                                                                                                                                                  Cucurbita pepo.
                                                                                                                                                                                                                                                                                                                                                                                               (NIHA ) JAPAN
                                                                                                                                                                                                                                                                              JP09163987-A
                                                                                                                                                                                                                                                                                                                                      14-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                 14-DEC-1995;
                                                                                                                                                                                                                                                                                                           24-JUN-1997.
                                                                                                                                                  10-0CT-1997
                                                                                                                                                                               Chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                      AAW24554;
                                                                                                                                                                                                                                                                                                                                                                                                              (SEKI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                RESULT 1
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TG------CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGDLDIRKREVAAFFGQISHEIIGGWPIAPDGPFSWGYCFKQEQGSPPSYC-DQSADWP 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAPG-KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 CATAVLAVALAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This recombinant tobacco chitinase gene prod. is encoded by a genomic clone, lambda CHN17 which comprises 3 exons and has 5. and 3. untranslated regions. A fragment (claimed) from the 5.-untranslated region can be used to increase the expression of foreign genes in transgenic plants. The fragment is linked to a foreign gene, eg chitinase or glucanase gene via a spacer and is also linked to regulatory sequences. The resultant DNA construct is used to transform plant cells, eg tomato, or tobacco, which subsequently produce the gene prod.
240 gygvitniingglecgrgadsrvadrigfykrycdllgigygnnldcnngrsf 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA regulatory sequence from new tobacco chitinase gene used to increase expression of foreign genes in transgenic plants, partic for improving resistance to pathogens etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                           Plant chitinase; transgenic plants; pathogen resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                    Chitinase encoded by genomic clone lambda CHN17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1161; DB 1
Pred. No. 1e-90;
4; Mismatches (
                                                                                                                                                                   A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; page 44; 65pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neuhaus J-M;
                                                                                                                                         AAR11305
ID AAR11305 standard; Protein; 331
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63.2%;
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                                                                                                                                                                                                                                                                                  (first entry)
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251 TPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDC 310
                                                                               IQLTHNYNYGPAGRAIGYDLLNNPDLYATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLW 250
                                                                                            VAAFFGQTSHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGP 190
||| | || || 303 yngrpfgngl 312
                                                                                                                                                                                 311 YNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                            15
                                                                                     191
                                         131
                                                                                                                                                                                                                                                     AAR20822
                                                                                                                                                                                                                                            RESULT
                                                                                     QΥ
                                                                                                            g
                                                                                                                                     Qγ
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                                                                                                                                                                                 Q\underline{Y}
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                                         Qy
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         184 capgrrkyfgrgpiqishnynygpcgraigvdllnnpdlvatdpvisfksalwfwmtpgs 243
                                             297
                                 NKPSCHDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated chitinase gene derived from an American elm - used to obtain prods, for inhibiting fungal infection of plants
                                                                                                                                                                                                                                                       ; american elm; fungus; Ophiostoma ulmi; coli; chitinase-like protein;
                                                                                                                                                                                                                                                                                                                                                                          "Mature chitinase-like protein"
                                                                                                                                                                                                                                                                                                                                            /note= "signal peptide" 22..317
/note= "Mature chitinas
                                                                                                                                                                                                                                   American elm chitinase-like protein.
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                               AAW00186 standard; Protein; 317 AA
                                                                               298 DIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                              silgvspgdnldcgnqrsfgngl 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Fig 1; 12pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94US-0286020
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                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sticklen MB;
                                                                                                                                                                                                                                                          chitinase;
                                                                                                                                                                                                                                                                     disease; E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-353879/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 AA;
                                                                                                                                                                                                                                                                                fungal infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAT33325
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                                                                                                                                                                                                                                                                                                        American elm
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dutch elm di
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                                                                                                                                                                                                             18-0CT-1996
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                                                                                                                                                                                       AAW00186;
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Peptide
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The inventors claim a new recombinant gene which codes for a protein with encochitinase activity, or its precursor (see AAQ21007). The coding part of the gene contains at least the 5' part of DNA for tomato enzyme (DNA can be genomic or cDNA, but at least one intron is prefigresent). The recombinant gene includes the 35s promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of Agrobacterium tumefaciens.
                                                                                       Pest-resistant plant; transformed plant; fungi; insect; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                        New recombinant protein with endo chitinase activity - also DNA encoding it and plants which express it, resistant to fungi, insects, bacteria and nematodes.
                                                                                                                                                                                                                                                                                                                                                     Toppan A;
                                                                                                                                                                                                                                                                                                                                                     Pignard A,
                                                                    endochitinase procursor.
                                                                                                                                                   Location/Qualifiers
AAR20822 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                     Leguay JJ,
                                                                                                                                                                                   25..69
/label= cleavage
                                                                                                                                                    1..24
/label= signal
25..69
                                                                                                                                                                                                                                                                                                                   (SNFI ) SANOFI SA.
(ERAP ) SOC NAT ELF AQUITAINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example; Fig 4; 82pp; French
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                                               (first entry)
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N-PSDB; AAQ21193.
                                                                                                                               Fomato and tobacco.
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                                               16-MAY-1992
                                                                     Sequence of
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                        AAR20822;
                                                                                                         nematode
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Indels

Length 317;

DB 17;

Score 1160; DB 17 Pred. No. 1.2e-90; Mismatches

64.7%; 65.8%;

33;

Conservative

204;

Similarity

Local

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Query Match

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                                                                                                          66 CTGCGGG-----GGGVASIVSRDLFERFILLHRNDAACLAR-GFYTYDAFLAAAGAFPAFG 119
                                                                         7 RCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLOCSQEGFGGTTSDYCGP-RQQSQ 65
                                          Gaps
 DB 13; Length 328;
                 66; Indels
Query Match 63.8%; Score 1142.5; DB Best Local Similarity 60.4%; Pred. No. 3.7e-89; Matches 194; Conservative 54; Mismatches 66
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum DB seq
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Perfect score:
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28 818.5 45.7 254 1 US-08-047-413-9 Sequence 9, Appli 29 B18.5 45.7 254 3 US-08-229-050-9 Sequence 9, Appli 30 B18.5 45.7 254 3 US-08-229-050-9 Sequence 9, Appli 31 B09 45.1 253 1 US-08-162-475A-5 Sequence 5, Appli 32 784 43.8 253 4 US-07-791-931-9 Sequence 9, Appli 33 781.5 43.6 253 1 US-08-162-475A-2 Sequence 9, Appli 34 779.5 43.5 250 1 US-08-162-475A-4 Sequence 7, Appli 35 70.5 39.5 372 4 US-07-791-931-4 Sequence 7, Appli 36 70.5 39.5 372 4 US-07-791-931-4 Sequence 7, Appli 36 70.5 39.5 372 4 US-07-791-931-4 Sequence 37, Appli 38 232 12.9 51 3 US-08-329-799-35 Sequence 35, Appli 40 212 11.9 71 1 US-08-195-15 Sequence 15, Appli 41 212 11.8 71 1 US-08-37-259-15 Sequence 15, Appli 42 20.5 11.2 20.9 6 5187262-2 Sequence 14, Appli 44 200.5 11.2 20.9 6 5187262-2 Sequence 14, Appli 44 200.5 11.0 CS-08-935-886-8
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ALIGNMENTS

RESULT

SQUENCE 3, AAPLICATION US/07704288C

SQUENCE 3, AAPLICATION US/07704288C

PARCEL KE. 5395680

PARCEL KE. 5395680

SQUENCE 5, SQUENCES 5

SAPELICANT: LAMB, CHRISTOPHER J.

APPLICANT: LAMB, CHRISTOPHER J.

STREET: A44 SOUTH Flower Street, Suite 2000

CORRESPONDENCE ADDRESS:

COMPUTER: United States

STATE: California Forma:

COMPUTER: The COMPUTER: TOWN COMPATIBLE

COMPUTER: THE POOPY disk

MUDITH TYPE: THO OPPLY A STEEN FOR COMPATIBLE

COMPUTER: THO OPPLY STEEN FOR ST

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                                                                                                 118 PGFAAAGDADTUKREVAAFLAQTSHETTGGWATAPDGPYTWGYCFKEENGGAGFDYCQQS 177
                                                                                                                                                                                                                       235 TQSNKPSCHDVITGIWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68.6%; Score 1230; DB 1;
69.3%; Pred. No. 1.6e-103;
tive 31; Mismatches 55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-WAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370 ""
FILING DAWN.
                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-08-379-259-3
Sequence 3, Application US/08379259
Patent No. 5695939
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                 298 RYCDILGVSYGANLDCYSQ 316
                                                                                                                                                                                                                                                                                                       295 RYCDIFGIGYGNNLDCYNQ 313
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amino acid
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Best Local Similarity 69.3%
Matches 221; Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: United ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE:
US-08-379-259-3
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                                                                                        116 PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08093372
Patent No. 5530187
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lab, Qun
APPLICANT: Anher, Elleen A.
APPLICANT: Dixon, Richard A.
APPLICANT: TRANSGENIC PLANTS CONTAINING MULTIPLE TITLE OF INVENTION: TRANSGENIC PLANTS GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1230; DB 1;
Pred. No. 1.6e-103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
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TELEPHONE: 619-546-4737
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69.38;
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Best Local Similarity 69.3%
Matches 221; Conservative
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INFORMATION FOR SEQ ID NO:
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CLASSIFICATION:
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US-08-093-372-2
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STATE:
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US-08-229-050-11
                TOPOLOGY:
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APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT 234
                                                                                                                                                                                                                                           64 SQCT-----GCGGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF 115
                                                                                                                                             116 PAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS 174
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                                     57
   4 LEARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ
                                                                                                                                                                                                                                                                                            235 TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
CLASSIFICATION: 800
PRIOR APPLICATION: 800
PRIOR APPLICATION: 800
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: AND APPLICATION OF APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24615-20022.00
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APPLICANT: Melchers, Leo S.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Selar Buurlage, Marianne B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
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Patent No. 5670706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                          |||||| |: || |||||||||| RYCDILGVSYGANLDCYSQ 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 324 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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US-08-047-413-11
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APPLICANT: BOL, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLECTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       125 DIRKREVAAFFGQISHETIGGWPIAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQ 184
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                                                                                                                                                                                                                                                                                                    67 TG--CGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDL 124
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                                                                                             Query Match 65.7%; Score 1177.5; DB 1; Best Local Similarity 64.2%; Pred. No. 8.4e-99; Matches 203; Conservative 45; Mismatches 65;
                                                                                                                                                                                                   8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFC
                                                                                                                                                                                                                                           4 CKFTALSSLLFSLLLLSASAEQCGSQAGGARCASGLCCSKFGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cornelissen, Bernardus J.C. APPLICANT: Melchers, Leo S. APPLICANT: Melchers, Leo S. APPLICANT: Weulenhoff, Elisabeth J.S. APPLICANT: van Rockel, Jeroen S.C. APPLICANT: Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/229,050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Meulenhoff, Elisabeth J
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Sela-Buurlage, Marianne
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PC-DOS/MS-DOS
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STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/08229050
Patent No. 6066491
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MEDIUM TYPE: Floppy disk
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CITY: Palo Alto
, MOLECULE TYPE: protein US-08-047-413-11
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TYPE: PRT ORGANISM: Nicotiana tabacum
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LENGTH: 310
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Sequence 11, Application US/08801563
Patent No. 6087560
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Welchers, Leo S.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: van Roekel, Jeroen S.C.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 YYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHD 244
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                                                                                                                                                                                                                                                                                Length 324;
                                                                                                                                                                                                                                                                                65.7%; Score 1177.5; DB 3; Length.
64.2%; Pred. No. 8.4e-99;
.ive 45; Mismatches 65; Indels
NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REJECHNCE/DOCKET NUMBER: 24615-20022.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : Morrison & Foerster
755 Page Mill Road
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IBM PC compatible
                                                                                         TELEX: 415-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 324 amino acids
TYPE: amino acid
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                                                                                                                                                                                         ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-229-050-11
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CITY: Palo Alto
STATE: California
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Matches 203; Conserv
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244 VIIGRWQPSSADRAANRLPGFGVITNIINGGLECGRGTDSRVQDRIGFYRRYCSILGVSP 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 PGGPTPPGGGDLGSIISSSMFDQMLKHRNDNACQGRGFYSYNAFINAARSFPGFGTSGDT 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 3;
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                Version #1.25
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GENERAL INFORMATION:
APPLICANT: Raikhel, Natasha V.
TILE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
         OPERATING STORM:
COERREATING STORMS.
COERREAT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,563
FILING DATE:
CLASSIFICATION NUMBER: US/08/801,563
FILING DATE:
APPLICATION NUMBER: US 08/047,413
FILING DATE: 19-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, X4CH H.
REGISTRATION NUMBER: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, X4CH H.
REGISTRATION NUMBER: 24615-20022
REFERENCE/DOCKET NUMBER: 24615-20022
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
TELEFAX: 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
108-07-791-931-6
Sequence 6, Application US/07791931C
; Patent No. 6133507.
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amino acid
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Best Local Similarity 64.2%
Matches 203; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: protein US-08-801-563-11
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OPERATING SYSTEM:
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Best Local Similarity
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TITLE OF INVENTION: BLEMET BEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 SSMFDQMLKHRNDNACQGKGFYSYNAFINAARSFPGFGTSGDTTARKKEIAAFFAQTSHE 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
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                                                                                                                                                                                                                                                                                                                                                                                                       82 RDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                         Length 310;
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ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                 DB 4;
                                                                                                                             65.7%; Score 1176.5; DB 67.2%; Pred. No. 9.8e-99;
                                                                                                                                                                                                     41; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/07704288C Patent No. 5399680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/05
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RY: United States 90071-2921
                                                                                                                                 Query Match
Best Local Similarity 67.24
Matches 201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid STRANDEDNESS: unl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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US-07-704-288C-6
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                          US-07-791-931-6
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82 RDLFERFILLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHE 141
                                                                                                                                                 142 TTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
                                                                                                                                                                                                                          202 AGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
                                                                                                                                                                                                                                                                                                                                                   262 VPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                 25 ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTG--CGGGGGGVASIVS 81
                                                                            4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 310;
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: PRETIY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENY APPLICATION DATA: APPLICATION NUMBER: US/08/379,259 FILING DATE:
; Pred. No. 7.1e-98; 41; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.1%; Score 1167;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.508-379-259-6
; Sequence 6, Application US/08379259
; Patent No. 5695939
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   67.28;
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                       Matches 201; Conservative
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us-09-534-229c-2.rai

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APPLICANT: BUBGIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: GEGUAY, Dean-Jacques
APPLICANT: PIGNAD, Annie
APPLICANT: PIGNAD, Annie
APPLICANT: POPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                  177 WPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQ 236
                                                                                                                                                                                                                                                                                                                                                                                        SNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGONDKVADRIGFYKRY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SPKPSCHDVIIGRWNPSAGDRSANRLPGFGVITNIINGGLECGRGNDNRVQDRIGFYRKY 300
                                                                                                                                                                                                                 63 QSQCTGCGGG-----GGGVASIVSRDLFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFP 116
                                                                                                                                                                                                                                                  61 QSQCPGGGPGPGPVTGGDLGSVISNSMFDQMLKHRNENSCQGKNNFTSYNAFITAARSFP 120
                                                                                                                                                                                                                                                                                         117 AFGTIGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                                                                                                                                                                                              4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RC 62
                                                                                                      7;
                                                                   Length 329;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: FOLEY & LARDNER STREET: King Street Station, Suite 500,1800 Diagonal STREET: Road, PO Box 299 CITY: ALEXANDRIA
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                                                                     DB 2;
                                                                                                        69;
                                                                 63.7%; Score 1141.5; DB
59.9%; Pred. No. 1.5e-95;
Live 54; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 13, Application US/07842165; Patent No. 5932698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      297 CDIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28,665
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13:
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(703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                            Matches 194; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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 protein
                                                                         Query Match
Best Local Similarity
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; MOLECULE TYPE:
US-08-475-427-13
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                                                                                                                                                                                                                                                                                                    82 RDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHE 141
                                                                                                                                                       202 AGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
                                                                                                                                                                                                             142 TTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
                                                                                                                                                                                                                                                                                                                                                           262 VPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                247 LPGFGYITNIINGGLECGRGTDSRYQDRIGFYRRYCSILGVSPGDNLDCGNQRSFGNGL 305
                         Gaps
                                                                               25 ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTG--CGGGGGGVASIVS 81
                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
   Pred. No. 7.1e-98;
1: Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16781/564/BEDL
                       41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington, D.C. COUNTRY: USA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-UUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA_
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13, Application US/08475427 Patent No. 5859340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: GEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (202)672-5300
(202)672-5399
     67.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 329 amino acids TYPE: amino acid
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                           201; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
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         Best Local Similarity
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US-08-475-427-13
                             Matches
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us-09-534-229c-2.rai

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LTHNYNYGPACRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTP 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDLSALISRSTFDOMLKHRNDGACPARGFYIYDAFIAARAYPSFGNIGDTAIRKREIA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFFGQTSHETTGGWPTAPDGFFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS

TURBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGGG 72
                                   253 TARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYN 312
                                                    252 SSADVAARRLPGYGTVINIINGGLECGRGQDSRVODRIGFFKRYCDLLGYGYGNNLDCYS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 VGVVWMLLLVGGSYGEQCGRQAGGALCPGGNCCSQFGWCGSTTDYCGPGCQSQCGGPSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192 ISWNYNYGQCGRAIGVDLLNKPDLVATDSVISFKSALWFWMTAQSPKPSSHDVITSRWTP
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                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-223
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ve.
CURRENT APPLICATION DATA::
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/ALENT INFORMATION:
NAME: Red: Stephen E.
REG: STRATION UNIMBER: 31,192
REG: STRATION UNIMBER: 31,192
                                                                                                                                                                                                                                         Sequence 9, Application US/07704288C Patent No. 5399680
                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,192
REPERHOR/DOCKET NUMBER: P31
PELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEPRAX: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     318 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
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                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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196; Conserva
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                                                                                                                  313 QLSFNVGL 320
                                                                                                                                                       312 QTPFGNSL 319
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                                                                                                                                                                                                                                US-07-704-288C-9
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 AFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQ 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                                                                                                                                                                                                                                                                       236
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                                                                                                                                                                                                                                                                                        QSQCTGCGGG-----GGGVASIVSRDLFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                177 WPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQ
                                                                                                                                                                                                                  4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RC
                                                                                                                                                                                                                                     Length 328;
                                                                                                                                              Length 329;
                                                                                                                                                                                 69; Indels
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63.6%; Pred. No. 5.3e-95;
Live 44; Mismatches 67; 1
                                                                                                                                              DB 2;
                                                                                                                                          Query Match 63.7%; Score 1141.5; DB :
Best Local Similarity 59.9%; Pred. No. 1.5e-95;
Matches 194; Conservative 54; Mismatches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSV 4.1.114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SOFWARE: Patentin Ver. 2.0
SEQ ID NO 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/07791931C Patent No. 6133507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            297 CDIFGIGYGNNLDCYNQLSFNVGL 320
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US-07-791-931-7
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Best Local Similarity 63.6%,
Matches 196; Conservative
                   : 329 amino acids
AMINO ACID
                                                    ; TOPOLOGY: linear; MOLECULE TYPE: protein US-07-842-165-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                     LENGTH:
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                                                                                                               253 TARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYN 312
124 AFLGQTSHETTGGWATAPDGPYAWGYCFVRERN--PSTCSAĮPQFPCAPGQQYYGRGPIQ 181
                                                                                                                                242 SSADVAARRLPGYGTVTWIINGGLECGRGQDSRVQDRIGFFKRYCDLLGVGYGNNLDCYS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22 VIPATARQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCG---GGGGGVA 77
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                                                           Length 328;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
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Pred. No. 3.8e-94;
3; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: RAIKHA!.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002, 18:43:04
                                                                                                                                                                                                                                                                                                                           ; Sequence 5, Application US/07791931C; Patent No. 6133507
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illarity 62.7%;
Conservative 48
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Matches 190;
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-07-791-931-5
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SEQ ID NO 5
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                                                 253 TARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYN 312
                                                                         182 ISWNYNYGQCGRAIGVDLINKPDLVATDSVISFKSALWFWMTAQSPKPSSHDVITSRWTP 24.1
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; Pred. No. 2e-94;
42; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                    PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
FILING DATE:
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Relter, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 31,193
TELEPHONE: (619) 546-4137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         Sequence 9, Application US/08379259
Patent No. 565939
Patent No. 565939
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE REGULE
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.6%;
Matches 196; Conservative 42
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ADDRESSEE: r...
STREET: 444 South .
CITY: Los Angeles
"TATE: California
"TATE: United States
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TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 318 amino acids
TYPE: amino acid
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                                                                                                                                                                  QTPFGNSL 309
                                                                                                                              313 QLSFNVGL 320
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US-08-379-259-9
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11126 11087 1087 1087 1051 1051 1040 1002 988 988 9873 969.5	SULT 1 19979 1tinase (EC 3.2 Species Oryza Accession: 8399 Nishizawa, Y.; Nocession: 8399 Status: prelimi Mocesion: 8399 Nishizawa Nishiza	301 RIG
888888888844444 011884888888444444	Match 1	Dp 3
	SEES SEES SEES SEES SEES SEES SEES SEE	Ω

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C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Hordeum vulgare (baxley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243 SHAVITGQWSPSGTDRAAGRVPGFGVITNIVNGGIECGHGQDSRVADRIGFYKRYCDILG 302
                                                                                                                                                                  A; Residues: 1-318 <IGN>
A; Cross-references: EMBL: U02287; NID: 9495304; PIDN: AAA18586.1; PID: 9495305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSTPVTPTSGGGGVSIVSRALEDRMLLHRNDGACQARGFYTYDAFVAAASAFRGFGTT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             182 GKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFG 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------GGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                         256 DSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLS 315
                                                                                                                                                                                                                                                                                                                                                                                           VASIVSRDLFERFILHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                NYNYGPAGRAIGYDLLANNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTAR
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                                                                                                                                     GQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Keywords: glycosidase, hydrolase, polysaccharide degradation C,Keywords: glycosidase, hydrolase, polysaccharide degradation F;1-19/Domain: signal sequence #status predicted <SIG>P;20-318/Product: chtinase #status predicted <MAI>F;20-60/Domain: hevein chitin-binding domain homology <HCB>P;80-318/Domain: plant chitinase homology <PCH>
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Pred. No. 4.4e-92;
7; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable chitinase (EC 3.2.1.14) precursor - barley C; Species: Hordeum vulgare (barley)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C'Accession: T04403
S'Ignatius, S.M.J.; Huang, J.; Muthukrishnan, S.
submitted to the EMBL Data Library, September 1993
A,Description: Isolation and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDBJ
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74.08;
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Matches 233; Conserv
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chitinase (EC 3.2.1.14) - rice
C;Species: Orgza sativa (rice)
C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S40414
R;Nishizawa, Y.
Submitted to the EMBL Data Library, November 1990
A;Reference number: S40414
A;Recession: S40414
A;Accession: S40414
A;Accession: S40414
A;Accession: S40414
A;Accession: S40414
A;Accession: S40414
A;Accession: J-340
A;Experimentary
A;Molecule type: mRNA
A;Residues: 1-340
A;Cross references: EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407472
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p1
C;Superfamily: hevein chitinase homology <PCH>
F;92-330/Domain: plant chitinase homology <PCH>
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chitinase (EC 3.2.1.14) a - rye
C;Species: Secale cereale (rye)
C;Species: Socale cereale (rye)
C;Species: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C;Accession: JC2071
R;Yamagami, T.; Funatsu, G.
Biosci. Biotechnol. Biotech
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDA 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.4%; Score 1315; DB 2;
76.1%; Pred. No. 1.8e-93;
iive 24; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DRIGEYKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.0%; Score 1326.5; DB 70.9%; Pred. No. 2.6e-94; iive 29; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 76.1 tes 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 70.95
Matches 241; Conservative
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probable chitinase (EC 3.2.1.14) precursor - rice c.5pecies: Oryza sativa (rice) C.5pecies: Oryza sativa (rice) C.5pecies: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000 C.5cession: 170329 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000 C.Accession: T0329 R.Anuratha, C.S.; Mew, T.; Muthukrishnan, S. submitted to the EMBL Data Library, September 1993 A.5meription of chitinases and beta-glucanases in Rhizoctonia solani infe A.Accession: T03239 A.Accession
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A. Experimental source: leaf, strain IRS8
C. Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C. Keywords: glycosidase; hydrolase; polysaccharide degradation
F. J. S. Domain: signal sequence #status predicted < NG>
F. 33 - 335/Froduct: chitinase #status predicted < NAL>
F. 33 - 74/Domain: hevein chitin-binding domain homology < HCB>
F. 90 - 325/Domain: plant chitinase homology < PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 YCQPFAGWPCAPGRKYYGRGPIQLSFNFNYGPAGRAIGVDLLSNPDLVATDATVSFKTAL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFL 109
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                                                                                                                                                                                                                                                                                                     245 SHDVITGRWSPSGADQAAGRVPCYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG 304
                                                                                                                                                                                                                                                              72 G------GGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                                                                                                                                                                                                                                                                                                                                                                   122 GDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFG 301
                                                              Gaps
                                                                                                                             VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
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Score 1283; DB 2;
Pred. No. 5.2e-91;
                                                                     34; Mismatches
   71.6%;
70.5%;
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                                                                     Matches 222;
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Best Local Si
Matches 237;
          Query Match
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                                                                                                                                                                           C,Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
C;Accession: T04484
Fibah, R: Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Plant J. 6, 579-589, 1994
A;Title: Identification of an enhancer/silencer sequence directing the aleurone-specific A;Reference number: 215373; MUID:95078949
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A)Cross-references: EMBL:X76041; NID:9416028; PIDN:CAA53626.1; PID:9416029
C)Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F)21-62/Domain: hevein chitin-binding domain homology <HCB>
F)21-62/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                           A) Accession: T04484
A) Status: preliminary; translated from GB/EMBL/DDBJ
A) Molecule type: DABA
A) Molecule type: DABA
A) CLGA
A) Cross-references: EMBL:134211; NID:9576566; PIDN:AAA56787.1; PID:9507961
C) Genetics:
A) Genetics:
C) Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C) Keywords: glycosidase; hydrolase; polysaccharide degradation
E) 28-69/Domain: hevein chitin-binding domain homology <HCB>
E) 85-322/Domain: plant chitinase homology <PCH>
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 22-Jun-1999
                                                                                                                                           Species: Hordeum vulgare (barley)
Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 TIGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 PSSHAVITGQWTPTAADTAAGRVPGYGVITNIINGGLECGRGADSRVADRIGFYQRYCNI 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CG-----GGGGGVASIVSRDLFERFILHRN---DAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 AIVAIVLSAALAMAMVVRAQQCGSQAGGATCPNCLCCSRFGYCGSTSDYCGAGCQSQCSG 68
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Pest Local Similarity 71.0%; Pred. No. 2.4e-91;
Matches 230; Conservative 35; Mismatches 44; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reisener,
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R;Liao, Y.C.; Kreuzaler, F.; Tiburzy, R.; Reisener submitted to the EMBL Data Library, November 1993
A;Reference number: S38670
A;Accession: S38670
A;Status: preliminary
A;Molecule type: DNA
                                                                                       probable chitinase (EC 3.2.1.14) - barley C; Species: Hordeum vn. / אבריביר
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                305 LGVGYGGNLDCYNORPFVEGLLIQ 328
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9

Gaps

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chitinase (EC 3.2.1.14) - rice
NyAlternate names: class I endochitinase
C;Species: Oryza sativa (rice)
C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S14948
R;Huang, J.K.; Nen, L.; Swegle, M.; Tran, H.C.; Thin, T.H.; Naylor, H.M.; Muthukrishn
Plant Mol. Biol. 16, 479-480, 1991
A;Reference number: S14948; MUID:91370895
A;Retssion: S14948; MUID:91370895
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-318 <-MANA
A;Residues: 1-319 <-MANA
A;Resid
                                                                                                                                       A Residues: 1-336 <MOL>
C Superfamily: lectin-related plant chitinase, hevein chitin-binding domain homology; C; Superfamily: lectin-related plant chitinase; polysaccharide degradation C; Keywords: glycosidase; hydrolase; polysaccharide degradation F; 22-63/Domain: hevein chitin-binding domain homology <HCB>
F; 22-63/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   homology;
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C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain
C; Keywords: glycosladase; hydrolase; polysaccharide degradation
F:19-60/Domain: hevein chitin-binding domain homology <HCB>
F:79-316/Domain: plant chitinase homology <PCH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---GCGGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAF 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 -----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGD 123
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MRALAVVAMVARPFLAAAV~~~HAEQCGSQAGGAVCPNCLCCSQFGWCGSTSDYCGAGCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAPGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ-GSPPSYCDQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
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                                                                                                                                                                                                                                                                                                                                                               Score 1230; DB 2;
Pred. No. 6.2e-87;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
number: S15997; MUID:91238706
: S15997
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Best Local Similarity
Matches 221; Conserv
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les 218; Conserv
                                                                            A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <MOL>
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                                                     A; Accession:
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Matches
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NiAlternate names: endochitinase
Cippecies: Oryza sativa (rice)
Cipate: 24-War-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
Rishizawa T. Stabination, differential expression and chromosomal location of rice changed factor number: 339979; MUID: 94049667
A; Reference number: 339979; MUID: 94049667
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Residuces: 1-333 < ALS
A; Residuces: 1-333 < ALS
A; Residuces: 1-332 < ALS
A; Residuces: 1-332 < ALS
A; Residuces: Cit-1
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Reywords: glycosidase; hydrolase
F; 21-62/Domain: hevein chitin-binding domain homology < RCB>F; 82-322/Domain: plant chitinase homology < PCH>
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C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C;Accession: S1599; #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C;Accession: S1599; #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
B;Zhu, Q: Lamb, C.J.
Mol. Gen. Genet. 226, 289-296, 1991
A;Title: Isolation and characterization of a rice gene encoding a basic chitinase.
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                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 SCGGGGPTPPSGGGGSGVASIVSRSLFDQMLLHRNDAACPAKNFYTYDAFVAAANAFPSF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ----GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK 294
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                                                                                  240 WFWMIPQGNKPSSHDVVIGRWAP-RRDVAAGRA-GYGVITNIVNGGLEGGDGPDDRVANR
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C;Accession: S65019
R;Beerhues, L.; Kombrink, E.
Plant Mol. Biol. 24, 353-367, 1994
A;Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-b
A;Reference number: S43317; MUID:94154255
A;Accession: S65019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: EMBL:X87109; NID:g807954; PIDN:CAA60590.1; PID:g807955 C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C; Keywords: glycosidase; hydrolase; polysaccharide degradation E; 21-62/Domain: hevein chitin-binding domain homology <FCB> F:21-62/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                     A;Cross-references: EMBL:U02605; NID:9467819; PIDN:AAA18332.1; PID:9467820 C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Keywords: glycosidase; hydrolase c;Keywords: glycosidase; hydrolase E;19-61,Domain: hevein chitin-binding domain homology <HCB> F;71-310/Domain: plant chitinase homology <PCH>
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C;Species: Oryza sativa (rice)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: S65771; S54806
R;Xu, Y; Zhu, Q.; Panbangred, W.; Shirasu, K.; Lamb, C.
Plant Mol. Biol. 30, 387-401, 1996
A;Title: Regulation, expression and function of a new basic chitinase gene.
A;Reference number: S65771; MUID:96189256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 GVASIVSRDLFERFLLHRNDAACLARG-FYTYDAFLAAAGAFPAFGTTGDLDTRKREVAA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67 DLGGYISNSMFDQMLNHRNDNACQGKGNFYSYNAFISAAGSFPGFGTTGDITARKREIAA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 FFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHNYNYGPCGRAIGVDLLNNPDLVATDSVISFKSAIWFWMTPQSPKPSCHDVITGRWQPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 THNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 ARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ
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67.2%; Pred. No. 4.8e-84;
Live 30; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                 66.6%; Score 1193;
66.8%; Pred. No. 4e
:ive 42; Mismatche
                                                                                                                                             A,Status: preliminary, translation not shown
A,Molecule type: mRNA
A,Residues: 1-318 <BEE>
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Best Local Similarity 67.23
Matches 217; Conservative
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-322 <XUZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 LSFNVGL 320
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S54806
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Cispecies: Pisum sativum (garden pea)
Cispecies: D. culley, D. days beas in citation 03-Nov-1995 #text_change 22-Jun-1999
Ciscession: S56694
R;Chang, M.M.; Horovitz, D.; Culley, D.; Hadwiger, L.A.
Plant Mol. Biol. 28, 105-111, 1995
A;Title: Molecular cloning and characterization of a pea chitinase gene expressed in rest A;Reference number: S56694; MuID:95306779
A;Accession: S56694
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <CHABL:137876; NID:9598346; PIDN:AAA75196.1; PID:9598347
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; p]
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology <R;21-62/Domain: hevein chitinase homology <PCH>
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C;Species: Solanum tuberosum (potato)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RCQSQCTGCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
                                                                 242
                                                                                                                                                                                                                                          242 HAVITGQWTPSADDQAAGRVPGYGETTNIINGGVECGHGADDKVADRIGFYKRYCDMLGV 301
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                                         LDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQE-QGSPPSYCDQSADWPCAPG 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSTLRARCATAVLAVVLAAAAVTPATABQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP
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                                                                                                                                                           HDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI
                                                                                                                               KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC
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Best Local Similarity
Matches 211; Conserv
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T07838
chitinase (EC 3.2.1.14) - cucurbit
C; Species: Cucurbita sp. (cucurbit)
C; Date: 14-May-1999 #text_change 20-Jun-2000
C; Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 20-Jun-2000
C; Accession: T07838
R; Baaka, M.
Submitted to the EMBL Data Library, June 1998
A; Accession: T07838
A; Accession: T07838
A; Accession: T07838
A; Molecule type: mRNA
A; Residues: 1-31 cESA>
A; Cross references: EMBL:AB015655; PIDN:BAA31131.1
C; Genetics:
A; Gene: chitpl
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C; Keywords: q14pcosidase; hydrolase; polysaccharide degradation
C; Keywords: q14pcosidase; hydrolase; polysaccharide degradation
F; 20-61/Pommain: hevein chitin-binding domain homology <PCH>
F; 75-311/Domain: plant chitinase homology <PCH>
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                                                                                    239 PQSPRPSCHAVMIGQWIPNGNDQAAGRVPGYGYVINIINGGVECGHGADSRVADRIGFYK 298
                                                                                                                               175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 IVLAFAEVLGAAAEQCGRQANGALCPNRLCCSQFGWCGNTDEYCKNNCQSQCTPPSTGGG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGP
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                     62 QLRRRRPDRPSGGGSGVASIVSRSLFDQMLLHRNDAACPAKNLYTYDAFVAAANAFPTF
                                                                                                                                                   235 TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
--GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAF
                                                                  -GSPPSYCDQS
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                                                                GITGDLDIRKREVAAFFGQISHEITGGWPIAPDGPFSWGYCFKQEQ--
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69.0%; Pred. No. 1e-83;
:ive 31; Mismatches
                                                                                                                                                                                                                                                                                      299 RYCDMLGVSYGANLDCYNQRPFN 321
                                                                                                                                                                                                                                                                 295 RYCDIFGIGYGNNLDCYNQLSFN 317
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Best Local Simi:
Matches 211;
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3, 2002, 18:32:12

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chitinase (EC 3.2.1.14) chi9 precursor - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 10.58p-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: 537344; 538838; 525637
R;Danhash, N.; Wagemakers, C.A.M.; van Kan, J.A.L.; de Wit, P.J.G.M.
Plant Mol. Biol. 22, 1017-1029; 1993
A;Title: Molecular characterization of four chitinase cDNAs obtained from Cladosporiu A;Reference number: 537341; MuID: 94003061
A;Accession: 537344
A;Molecule type: mRNA
A;Residues: 1-32 cDAN1>
A;Cross-references: EMBL:215140; NID: 919190; PIDN: CAA78845.1; PID: 919191
A;Accession: 53893
A;Accession: 53893
A;Accession: 53893
A;Molecule type: protein
A;Residues: 23-42;202-216;224-236;247-258 cDAN2>
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Keywords: 91ycosidase; hydrolase; polysaccharide degradation
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-322/Product: chitinase chi9 #status experimental <AMI>F;23-65/Domain: hevein chitin-binding domain homology <PCE>F;23-65/Domain: plant chitinase chi2 #status predicted <PCE>F;23-65/Domain: plant chi1inase chi2 #status predicted <PCE>F;23-65/Domain: plant chi2 #stat
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

May 3, 2002, 18:48:31; Search time 78:59 Seconds (without alignments) 150.690 Million cell updates/sec

Run on:

US-09-534-229C-2 1792 1 MSTLRARCATAVLAVVLAAA.....rGNNLDCYNQLSFNVGLAAQ 323

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

100059 100059 segs, 36664827 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	955 hordeum	oryza	oryza	pisum sa	P52403 solanum tub	Q05538 lycopersico	P24091 nicotiana t	nicotia		solanum	Q41596 theobroma c	Q39799 gossypium h	P19171 arabidopsis	Q09023 brassica na	P36907 pisum sativ		Q39785 gossypium h	>	a	phaseolu	Solanum	P52406 solanum tub		, ,	Q05537 lycopersico	,	Q05540 lycopersico	P29021 petunia hyb		⊆	Ä	~	ŭ
SUMMARIES	QI	- 1	- 1	CHI1_ORYSA	CHI2_PEA	CHI1_SOLTU		CHI2_TOBAC	CHIL_TOBAC	CHI3_SOLTU	CHI2_SOLTU	CHI1_THECC	3	- 1	CHI2_BRANA	- 1	CHI3_TOBAC	CHI2_GOSHI	CHIB_VITVI	CHIT_PHAVU	CHI5_PHAVU	CHIT_SOLTU	CHI4_SOLTU	CHI2_HORVU	CHI6_POPTR	CHID_LYCES	CHIB_POPTR	. 1	CHIT_PETHY		CHIP_TOBAC	- 1	CHIA_LYCES	CHI8_POPTR
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dР	Query Match	72.4	9.89	68.0	8.99	9.99	66.1	66.1	62.8	65.7	65.5	65.1														53.2								
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AGI_URTDI CHIP_BETVU	CHIB_MAIZE CHIA_MAIZE	CHI4_BRANA	CHIT_DIOJA	CHIC_POPTR	IAMY_COILA	WINZ_SOLTU	CHI4_ARAHY	CHIB_ARAHY
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372	269	268	250	121	133	211	46	46
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707.5	585	528.5	500.5	279.5	266	210.5	208	194
3.5	3.4	38	40	41	42	43	44	45

ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 GSTPVTPIPSGGGGVSIVSRALFDRMLHRNDGACQAKGFYTYDAFVAAASAFRGFGTT 122
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CHITINASE_19_2; 1. idase; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GIUCCSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Mkaryota, Viridplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 GKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS
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!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zhu Q., Lamb C.J.; "Isolation and characterization of a rice gene encoding a basic
                                                                                                                                                                                                                                                                                                                                      12;
                                                                 POTENTIAL.
26 KDA BUDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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42D62B2FE8041954 CRC64;
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01-MAY-1992 (Rel. 22, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14)
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MEDLINE=91238706; PubMed=2034221;
                                                            318 2 62 C 52 43 B 43 B 57 57 83 3402 MW;
                                                                                                                                                                                                                                                                                                                                   Matches 233; Conservative
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    Multigene family.
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HSSP; P23951; 2BAA.
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318 AA;
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  PROSITE; PS00774;
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AC CHIZ_ORYSA
AC 01-MAY-1992
DT 01-MAY-1992
DT 01-DEC-1992
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GN RCH10.
OS OTYZA SALIVA
OC EUKATYOTA; VALUE
OC EUKATYON
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238 PQSPRPSCNAVATGQWTPSADDQRAGRVPGYGVITNIINGGLECGHGEDDRIADRIGFYK 297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 PGFAAAGDADTNKREVAAFLAQTSHETTGGWATAPDGPYTWGYCFKEENGGAGPDYCQQS 177
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STRAIN=CV. JAPONICA; TISSUE-Seedling;
MEDLINE=91370895; PubMed=1893114;
Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
Muthukrishnan S., Reeck G.R.;
"Nucleotide sequence of a rice genomic clone that encodes a class I
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pram; PF00182; Glyco_hydro_19.
Pram; PF00182; Glyco_hydro_19.
ProDom; PD000574; CHITINBINDNG.
ProDom; PD00069; Chitin_bind; 1.
SWART; SW00270; ChtBD1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITMASE I PRECURSOR (EC 3.2.1.14).
0ryza sativa (Rice).
Braryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzeae; Oryzeae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 LRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
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CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W; 7F4EC12655DEA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.6%; Score 1230; DB 1; Length 336; 69.3%; Pred. No. 4.4e-87;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MM;
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Best Local Similarity
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Multigene family.
SIGNAL
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P24626;
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R FIRSP; PO2777; HIEW.
R HISSP: PO2777; HIEW.
R InterPro; IPR001002; Chitin_bind.
R InterPro; IPR001002; Glyco_hydro_19.
R Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
ProDom; PD0006574; Glyco_hydro_19; 1.
ProDom; PD0006574; Glyco_hydro_19; 1.
R PROSTIE: PS00076; CHITIN_BINDING; 1.
R PROSTIE: PS00773; CHITIN_BINDING; 1.
R PROSTIE: PS00774; CHITIN_BINDING; 1.
R PROSTIE: PS00774; CHITIN_BINDING; 1.
Hydrolase: Glycosidase; Chitin degradation; Chitin-binding; Signal;
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                                                CATALTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
SIMILARITY: BELONGS TO CHITINNES CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALTIC PRAT BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC
Plant Mol. Biol. 16:479-480(1991).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.0%; Score 1218; DB 1; Length 318; Best Local Similarity 70.1%; Pred. No. 3.5e-86; Matches 218; Conservative 31; Mismatches 50; Indels 1:
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CHITIN-BINDING (BY SIMILARITY)
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SIMILARITY.
8FD37913450CC7EB CRC64;
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Multigene f
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                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. ALCAN;
MEDLINE-95306779; PubMed=7787175;
Chang M.M., Horovitz D., Culley D., Hadwiger L.A.;
"Molecular cloning and characterization of a pea chitinase gene
expressed in response to wounding, fungal infection and the elloitor
chitosan.";
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Vad K., Mikkelsen J.D., Collinge D.B.;
"Induction, purification and characterization of chitinase isolated
"Induction, purification of chitinase isolated
"Induction of chitinase 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARIY: LELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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InterPro; IRR010025; Glyco_hydro_19.
Ffam; PF00182; chitin_binding; 1.
Ffam; PF00182; chitin_binding; 1.
From; PF00182; chitin_binding; 1.
FRINTS; PR00451; CHITINBINDNG;
ProDom; PB000574; Glyco_hydro_19; 1.
SMART; SM00270; CHITINBID; 1.
FROSITE; PS00773; CHITINSE_19_1; 1.
FROSITE; PS00774; CHITINSE_19_2; 1.
FROSITE; PS00774; CHITINSE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONTAINING FUNGAL PATHOGENS.
-!-CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- INDUCTION: FOLLOWING INFECTION WITH THE FUNGAL PATHOGEN
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SIMILARITY.
540F0DA5EC1DC2FA CRC64;
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                                                                     01-MAY-1991 (Rel. 18, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
101-ULT-1999 (Rel. 38, Last annotation update)
ENDOCHITINASE A2 PRECURSOR (EC 3.2.1.14).
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
    PRT;
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HSSP; P02877; 1HEV.
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34678 M
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SIGNAL 1 20
    STANDARD;
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                                           3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- CATALYTIC ACTIVITY: HYDROLYGIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-!- DEVELOPMENTAL STAGE: HIGHEST LEAVES IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TO INFECTION, ELICITOR, ETHYLENE, WOUNDING
                                                                                                                                   61 RCQSQCTGCGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGT 120
                                                                                                                                                      IGDLDTRKREVAAFFGQTSHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCA 180
                                                                                                                                                                                                                            113 KGDTATKKREIAAFLGQTSHETTGGWPTAPDGPYAWGYCFLREQ-NPSTYCQASSEFPCA 171
                                           Gaps
                                                                       1 MSTLRARCATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-CV. DATURA; TISSUE-Leaf;
MEDLINE-94154255; PubMed-8111037;
MEDLINE-94154255; PubMed-8111037;
MEETHURE L., Kombinik B.;
"Primary structure and expression of mRNAs encoding basic chitinase and 1.3-bera-glucamase in potato.";
Plant Mol. Biol. 24:353-367(1994).
-1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Solanum tuberosum (Potato).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; eusterids I; Solanales; Solanaceae; Solanum.
                                                                                             1 MSKLR------IPILLVLFIVSCCSAEQCGTQAGGALCPGGLCCSKFGWCGSTSEYCGD
                                                                                                                                                                                                                                                                          PGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKP
                                                                                                                                                                                                                                                                                                                        SCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIF
                                           6
            Length 324;
                                           58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-027-1996 (Rel. 34, Created)
01-027-1996 (Rel. 34, Last sequence update)
01-027-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
            DB 1;
           66.8%; Score 1196.5; DB 65.9%; Pred. No. 1.5e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 AA.
                                          42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLD ROOT SEGMENTS, AND CARPELS. INDUCTION: IN RESPONSE TO INFEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                  GIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                       292 GIGYGDNLDCYSQRPFGSSL 311
                                          Matches 211; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asteridae; euast
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIL_SOLTU
P52403;
            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 5
CHI1_SOLTU
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253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eŭkaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Spernatophyta, Magnoliophyta, eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 FFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 VLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TARGETING (POTENTIAL).
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A0B49DA528706AAA CRC64;
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01-JUN-1994 (Rel. 29, Last sequence update)
01-CT-1994 (Rel. 30, Last annotation update)
BASIC 30 KDA ENOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.6%; Score 1193; DB 1;
66.8%; Pred. No. 2.8e-84;
live 42; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
ENDOCHITINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                     InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
ProDom; PP00182; Glyco_hydro_19; 1.
ProDom; PD000609; Chydro_19; 1.
PROSITE; SM0270; ChtBD1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00774; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60
36
42
B3
49
58
33813 MW;
U02605; AAA18332.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18
311
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 205; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase, Glycosi
Multigene family.
NON_TER 1
SIGNAL <1
CHAIN 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19
21
30
35
54
318 /
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NCBI_TaxID=4081;
[1]
                                      P23951;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             134 FFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Clivc_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pram; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000674; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
SWART; SW00270; ChtBDI, 1.
PROSITE; PS00773; CHITIN_BINDING; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
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                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIFSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGNTNEYCGPGNCQSQCPGGPGPSG
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
STRAIN=CW. MONEYMAKER;
MEDLINE=94003061, PubMed=8400122,
Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
Molecular characterization of four chitinase cDNAs obtained from Cladosporium fulvum-infected tomato.";
Plant Mol. Biol. 22:1017-1029(1993).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 VLAAAAVIPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGGG
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C3
                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REMOVED IN MATURE FORM.
CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASIC 30 KDA ENDOCHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
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Pred. No. 1.2e-83;
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SIMILARITY.
SIMILARITY.
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BY SIMILARITY.
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BY SIMILARITY.
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SIGNAL
1 22
CHAIN 23 315 BASIC
CHONAIN 23 64 CHITIN
DISULFID 25 40 BY SIM
DISULFID 39 53 BY SIM
MOD_RES 66 66 HYDROX
MOD_RES 68 68 HYDROX
SEQUENCE 322 AA; 34345 MW; D132
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66.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; Z15140; CAA78845.1; -.
PIR; S37344; S37344.
HSSP; P23951; 2BAA.
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                                                                                                                                                                                                                                                                                                                                                             HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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Matches
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Shinshi H., Mohnen D., Meins F. Jr.; "Regulation of a plant pathogenesis-related enzyme: inhibition of chitinase and chitinase mRNA accumulation in cultured tobacco tissues
                                                                                                     191 SHNYNYGPCGRAIGVDLLNNPDLVATDPVISFKSAIWFWMTPQSPKPSCHDVITGRWQPS 250
                                                                       254 ARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     van Buuren M., Neuhaus J. M., Shinshi H., Ryals J., Meins F. Jr.; mrthe structure and regulation of homeologous tobacco endochithnase genes of Nicotiana sylvestris and N. tomentosiformis origin."; Moi. Gen. Genet. 232.460-469(1992).
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-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-!- INDUCATION: BY ETHYLENE.
-!- SIMILARIY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana. NCBL_maxID-4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukuda Y., Ohme M., Shinshi H.;
"Gene structure and expression of a tobacco endochitinase gene in suspension-cultured tobacco cells.";
Plant MOI. Biol. 16:1-10(1991).
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SEQUENCE OF 15-324 FROM N.A., AND SEQUENCE OF 24-53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (CHN-B).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    324 AA
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STRAIN=CV. BRIGHT YELLOW 4; TISSUE=Leaf;
MEDLINE=91363829; PubMed=1888889;
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STRAIN-CV. HAVANA 425; TISSUE-Leaf;
MEDLINE-92269767; PubMed=1588915;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                             314 LSFNVGL 320
                                                                                                                                                                                                                                                                                     311 RSFGNGL 317
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P24091;
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CHI2_TOBAC
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329 AA.

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001002; Chitin_bind.

R InterPro; IPR001002; Chitin_bind.

R InterPro; IPR001002; Glyco_hydro_19.

Pfam; PF00187; Chitin_bind; 1.

Probom; P0000574; Glyco_hydro_19; 1.

Probom; P0000574; Glyco_hydro_19; 1.

RAART; SM00270; Chtbb1; 1.

RAART; SM00270; Chtbb1; 1.

RASTIE: P500773; CHITINABINDING; 1.

RR PROSTIE: P500774; CHITINASE_19_1; 1.

R PROSTIE: P500774; CHITINASE_19_2; 1.

R PROSTIE: P500774; CHITINASE_19_2; 1.

H Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Grank, Androlase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Grank, Androlase; Chitin_degradation; Chitin-binding; Signal; Chitin_degradation; Chitin_binding; Signal; Chitin_degradation; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 IGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCA 180
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CHITIN-BINDING (BY SIMILARITY).
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FA65DC2113B33EB6 CRC64;
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HYDROXYLATION.
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BMBL, X64519, CAA45822.1; --
BMBL, M1573; AAA34070.1; --
PIR, A29074, A29074.
PIR, S20981, S20981.
HSSP, P239512, 28AA.
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300 GVSPGDNLDCGNQRSFGNGL 319

RESULT 8 CHIL_TOBAC

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R HSSP; P23951; SDAA.

R HSSP; P23951; SDAA.

R HSSP; P23951; SDAA.

R InterPro; IPR000102; Chitin_bind.

R InterPro; IPR000102; Chitin_binding; 1.

R Ffam; PF00182; Glyco_hydro_19; 1.

R PRINTS; RR00451; CHITINBINDNG.

R ProDom; PD000609; Chitin_bind; 1.

R PROSTIE; PS00056; CHITIN_BINDING; 1.

R PROSTIE; PS000773; CHITINASE_19_1; 1.

R PROSTIE; PS00774; CHITINASE_19_1; 1.

R PROSTIE; PS00774; CHITINASE_19_2; 1.

R PROSTIE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CV. HAVANA 425; IISSUB=Leaf;
MEDLINE=91346623; PubMed=1966383;
Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr.;
"Structure of a tobacco endochitinase gene: evidence that different chitinase genes can arise by transposition of sequences encoding a cysteine-rich domain.";
                                                                                                                                                                                                          Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Epermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.

NCBL_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- FUNCTION: THIS PROPERTY FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-1- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GIJCOCSAMINE POLYMERS OF CHITIN.
-1- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-1- INDUCTION: BY ETHYLENE.
-1- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITINASE LIBROLY OF CHITINASE LOCATION OF CONTINUAL CON
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Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
A short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole.";
Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
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Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr
"Vacuolar chitinases of tobacco: a new class of hydroxyproline-
                                                                                      01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 14:357-368(1990).
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                                                      01-AUG-1988 (Rel. 08, Created)
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Science 257:655-657(1992).
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CHIL_TOBAC
P08252;
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CHIZ_SOLTU STANDARD; F
P52404;
01-OCT-1996 (Rel. 34, Created)
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33798 ]
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01; Conservative
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                                                                                                                                                                                                                                 67 TG-----CGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYIYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                           64 PGGPTPTPPTPPGGGDLGSISSSMFDQMLKHRNDNACQGKGFYSYNAFINAARSFPGFG 123
                                                                                                                                                                                                                                                                       120 TIGDLDIRKREVAAFFGQISHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC 179
                                                                                                                                                                                                                                                                                 239
                                                                                                                                                                                                                                                                                                                                                     240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                 and 1,3-beta-glicanse in potato.";
Plant Mol. Biol. 24:353-367(1994).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
-N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACOOLAR AND PROTOPLAST (BY SIMILARITY).
-!- DEVELOPMENTAL STRAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE
                                                                                                                                                                         Gaps
                                                                                                                                                                                            99
                                                                                                                                                                                                               63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=CV. DATURA, TISSUE=Leaf;
MEDLINE=94154255; PubMed=8111037;
Beerhues L., Kombrink E.;
"Primary structure and expression of mRNAs encoding basic chitinase
                                                                                                                                                                                                     180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                        8 CATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDXCGP-RCQSQC
                                                                                                                                                                                                                                                                                                                        ÷
        CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                     Length 329;
                                                                                                                                                                        65; Indels
                                                                                                            HYDROXYLATION (PARTIAL).
3EC99D96E6C0114C CRC64:
                                                         HYDROXYLATION (PARTIAL) HYDROXYLATION.
  REMOVED IN MATURE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0cT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                  Score 1181, DB 1;
Pred. No. 2.4e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   318 AA
                                                                                HYDROXYLATION.
                                                                                        HYDROXYLATION.
                                                                                                  HYDROXYLATION.
                                                                                                                                                                      44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                             300 FGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                          |: |:||| || || || || || || || || 324
                                                                                                                     MW.
                                                                                                                                                 65.9%;
329
441
441
653
663
667
771
772
35156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Potato)
                                                                                                                                                           Best Local Similarity Will Matches 204; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                   329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4113;
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P52405;
                                                                                               MOD_RES
MOD_RES
SEQUENCE
                                              DISULFID
MOD_RES
MOD_RES
MOD_RES
MOD_RES
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                    DISULFID
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SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                               OLD ROCT SEGMENTS, AND CARPELS.
-!- INDUCTION: IN RESPONSE TO INTECTION, ELICITOR, ETHYLENE, WOUNDING.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLIDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84 LFERFLLHRNDAACLAR-GFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHET 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 MFDQMLNHRNDNACQGKNNFYSYNAFISAAGSFPGFGTTGDITARKREIAAFLAQTSHET 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGRV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 IGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPA 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25 ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGP-RCQSQCTGCGGGGGGVASIVSRD 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001002; Chitin_bind.
InterPro; IPR007026; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
ProDom; PD000609; Chitin_bind; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 ASAEQCGSQAGGALCAPGLCCSXFGWCGNTNDYCGPGNCQSQCPGGPGGPGGDLGGVISNS 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 PGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       313
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CHTIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W: BF587A8515534E71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENDOCHITINASE 3. REMOVED IN MATURE FORM, VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.7%; Score 1177; DB 1;
67.4%; Pred. No. 4.7e-83;
tive 40; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       316 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U02607; AAA17409.1; -. HSSP; P23951; 2BAA.
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134 FFGQISHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQL 193

δ g δŽ d á q

194 THNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPT

185

7 LLFSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGNTNDYCGPGNCQSQCP--GGSPG 64 GVASIVSRDLFERFLLHRNDAACLARG-FYTYDAFLAAAGAFPAFGTTGDLDTRKREVAA

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TRAINGLOW, DATURA; ITSSUE-leaf;

RX MEDLINE=9415425; PubMed=8111037;

REATHWEST, CONTRINK E.;

RETAINARY STRUCTURE and expression of mRNAs encoding basic chitinase and 1,3-beta-glucanase in potato.";

Primary structure and expression of mRNAs encoding basic chitinase and 1,3-beta-glucanase in potato.";

Plant Mol. Biol. 24:533-367(1994).

CC -1- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.

CC -1- CATALATIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF NACETYL-D-GLUCOSAMINE POLYMBRS OF CHITIN.

CC -1- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: APPRECIABLE AMOUNTS ARE ALSO FOUND IN CC SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN CC 1- INDUCTION: IN RESPONSE TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CACCURACY.

CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CACCURACY.

CC CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CACCURACY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART: SM00270; ChtEbb.:
PROSITE: PS00026; CHITIN_BINDING; 1.
PROSITE: PS00773; CHITINASE_19_1; 1.
PROSITE: PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Multigene family. 1
SIGNAL <1 18 POTENTIAL.
                                                                  Solanum tuberosum (Potato).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMOVED IN MATURE FORM, VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81FB3DB3F222A0C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHITING (POTENTIAL).
CHITIN-BINDING (BY SIM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENDOCHITINASE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Glyco_hydro_19; 1.
ProDom; PD000609; Ghyco_hydro_19; 1.
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36
42
B3
49
B6
58
33629 MW;
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309
316
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                                                                                                                                                                               SEQUENCE FROM N.A.
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21
30
35
34
316 AA;
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PROPEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Snyder-Leiby T.E., Furtek D.B.;
"A genomic clone from Theobroma cacao L. with high similarity to plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHIIIN.
-!- SUBJULAR LOCATION: VACUOLAR AND PROPOPLAST (BY SIMILARITY).
-!- INDUCTION: IN RESPONSE TO INPECTION, ELICITOR, ETHYLENE, WOUNDING.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                            Theobroma cacao (Cacao) (Cocoa).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Theobroma.
                        254 ARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                class I endochitinase sequences.";
(In) Plant Gene Register PGR95-056.
-!- FUNCTION: THIS PROFEIN FONCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14)
                                                                                                                                                                                                                      321 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHTINBIRDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U30324; AAA80656.1; ...
HSSP; P02877; 1HEV.
Mendel; 1622; Thecc;Chial;1622.
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                                                                                                                                                                                                                STANDARD;
                                                                              314 LSFNVGL 320
                                                                                                                    305 RSFGNGL 311
                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3641;
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Q41596;
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Gaps

4;

65.5%; Score 1174; DB 1; Length 316; 66.1%; Pred. No. 7.8e-83; 1.ve 42; Mismatches 58; Indels

Conservative

Local Similarity

Query Match

203;

Matches

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                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
ENDOCHITINASE I PRECURSOR (EC 3.2.1.14).
60sSyptum hirsutum (Upland cotton).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Malvales; Malvaceae; Gossyptum.
                                                                                                                                                                                                                                                                                                                                                                     84 LFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFFGGTSHETT 143
                                                                                                                                                                                                                                                                                                                                                                                                                               144 G--GWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGP 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    202 AGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGR 261
                                                                                                                                                                                                                                                                                                           26 TAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPR--CQSQCTGCGGGGGGVASIVSRD 83
                                                                                                                                                                                                                                                                                                                                  20 SARQCGRQAGGALCPGGLCCSQFGWGNTDDYCKKENGCQSQCSGSGGDTGGLDSLITRE 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       262 VPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSFNVG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CV. COKER 201;
Levorson J.v., Chlan C.A.;
Lisotation of a genomic DNA clone from Gossypium hirsutum with high similarity to class I endochitinase plant sequences.";
(In) Plant Gene Register PGR96-054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycosidase; Chitin degradation; Chitin-binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-!- FUNCTION: DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
-!- CATALITIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLOOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                      9;
                                                                                                                                                                                                                                                 65.1%; Score 1166; DB 1; Length 321;
69.1%; Pred. No. 3.2e-82;
Live 33; Mismatches 53; Indels
                                                                POTEŇTIAL,
ENDQCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
                                                                                                          HINGE.
CATALYTIC.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, EB7DBFBC8D7A2ADB CRC64;
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   CHITINASE_19_1; 1.
CHITINASE_19_1; 1.
CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                      34847 MW;
                                                                                                                                                                                                                                                                              Conservative
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                                                             321
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                PS00773; (PS00774; (
                                                                                                                                                                                                                                                                Similarity
 PS00026;
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SEQUENCE FROM N.A.
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Matches 206;
                                                Hydrolase;
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Q39799;
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DISULFID
SEQUENCE
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GPAPGPGGLINLISRETFNQMLLHRNDGACPARGFYTYDAFIAAARSFPAFATTGDQATR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 KREVAAFFGQISHETIG--GWPTAPDGFFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQY 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 AVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCG-PRCQSQCTGC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                  Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 YGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 ITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYG
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                                                                                                                                                                                                                                                                                                                                                                                                               Length 324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         62; Indels
                                                                                                                                                                                                                                                                                                               BY SIMILARITY.
BY SIMILARITY.
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9923B123EFSC7E3E CRC64;
                                                                                                                                                                                                                                                                           ENDOCHITINASE 1.
REMOVED IN MATURE FORM (BY
                                                                                                                                                                                                                                                                                                                                                                                                          64.9%; Score 1163; DB 1;
65.5%; Pred. No. 5.5e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
BASIC ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      41; Mismatches
modified and this statement is not remove
entities requires a license agreement (So
or send an email to license@lsb-sib.ch).
                                                                 HSSP, P02877; 1HEV.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; clyco_hydro_19; 1.
PRINTS; PR00451; CHTINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000699; Chitin_bind; 1.
SWART; SN00270; ChtBD1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                      PROSITE; PS00026; CHTTIN_BINDING; 1. PROSITE; PS00773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_2; 1.
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34666 MW;
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01-FEB-1991 (Rel. 17, Last seq
15-JUL-1998 (Rel. 36, Last anno
                                                       EMBL; U60197; AAB67842.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 65.5
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NNLDCYNQSPEGNGVS 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  306 NNLDCYNQLSFNVGLA 321
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                                                                                                                                                                                                                                  Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                    324 AA;
                                                                                                                                                                                                                                             Multigene family SIGNAL
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                                                                                                                                                                                                                                  Hydrolase;
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PROPEP
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DISULFID
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA,
MEDLINE-20363099; PubMed=10907853;
Kaneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.;
"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl, TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-ACETYL-D-GLOCOSAMINE POLYMERS OF CHITIN.
SUBGELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
IISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL. IN ROOTS WITH LOWER LEVELS IN LEAVES AND PROTOPLASTS.
IISSUE SPECIFICITY: HIGH CONSTITUTIVE LEVEL. IN ROOTS WITH LOWER LEVELS IN LEAVES AND PLOWERING SHOOTS.
INDUCTION: ETHYLENE INDUCES HIGH LEVELS OF SYSTEMIC EXPRESSION OF BASIC CHITINASE WITH EXPRESSION INCREASING WITH PLANT AGE.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL HYDROLASES).
HYDROLASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                     Res. 7:217-221(2000),
FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF
                                                                                  Samac D.A., Hironaka C.M., Yallaly P.E., Shah D.M.; "Isolation and characterization of the genes encoding basic and acidic chitinase in Arabidopsis thaliana."; Plant Physiol. 93:907-914(1990).
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REMOVED IN MATURE FORM (PROBABL CHITIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See hor send an email to license@lsb-sib.ch).
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ProDom; PD000609; Chitin_bind; 1.
SWART; SW00270; ChtBll; 1.
PROSITE; PS0073; CHITIN_BINDIG; 1.
PROSITE; PS00773; CHITINARE_19_1; 1.
PROSITE; PS00774; CHITINARE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001002; Chitin_bind.
InterPro; IPR007026; Glyco_hydro_19.
Pfam: PF00187; Chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
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EMBL; AP002047; BAB03157.1; -.
HSSP; P23951; 2BAA.
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                                                          STRAIN-CV. COLUMBIA;
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HYDROLASES)
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                                                                                                                                                                                                                                        4;
                                                                                                                                                                                                                  Length 322;
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                     69;
                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                              Score 1154; DB 1;
Pred. No. 2.7e-81;
1; Mismatches 69
                                                                                                                                                                                                                                   34;
                                                                                                                                                                                                            64.48;
66.08;
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                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                208;
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CG---GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLD 125

69

TNLFLFLFFLFSLLLSLSSAEQCGRQAGGALCPNGLCCSEFGWCGNTEPYCKQPGCQSQCTP

Best Loca Matches

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246 IIGLWTPTARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYG 305
                                                                                                                                                                                             Eukaryota; Ŷiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDILINE-9414349; pubmed=8310072; Hamel F., Bellemare G.; Panel F., Bellemare G.; Mucleotide sequence of a Brasica napus endochitinase gene."; Plant Physiol. 101:1403-1403(1993).

-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF NACETYL-D-GICCOSAMINE POLYMERS OF CHTIN.

-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHTIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL).
                                                                  Chitin degradation; Chitin-binding; Signal;
                                                                                                          YGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDV
                                             TRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
ENDOGHITINASE CH25.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                            322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001002; Chitin bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam: PF00187; chitin binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRLWYS; PR00451; CHTTINBIRNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD00069; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS00026; CHITIN BINDING; 1. PS00773; CHITINASE_19_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00773; CHITINASE 19_1; PROSITE; PS00774; CHITINASE 19_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M95835; AAA32986.1; -.
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                        305 NNLDCYNQLSFNVGL 320
                                                                                                                                                                                                                                                                        GNLDCYNORSFVNGL 317
                                                                                                                                                                                                                                                                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322
62
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica napus (Rape)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eurosids II; Bra
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Multigene family.
SIGNAL
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21
23
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CHI2_BRANA
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                                                                                                                                                                                                                                                                                                                                                                                                                              63 IPPGPIGDLSGIISRSQFDDMLKHRNDNACPARGFYTYDAFINAAKSFPGFGTIGDTATR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 C-GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 KREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248 GLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pisum sativum (Garden pea).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Vicieae; Pisum.
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                             10 TAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYC-GPRCQSQCTG 68
                                                                                                                                                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                                                                                   SCELLFIFESFLESFSLAEQCGRQAGGALCPNGLCCSEFGWCGDFEAYCKQPGCQSQCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDUCTION: BY FUNGAL INPECTION.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVIT
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                                                                                                                                                                           Length 322;
                                                                                                                                                                                                                                Indels
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
: E62EE4B17211DBCD CRC54;
                                                                                                                                                                                                                                   68;
                                                                                                                                                                  64.0%; Score 1146; DB 1;
66.3%; Pred. No. 1.1e-80;
11ve 34; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
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44 B
51 B
60 B
34816 MW;
                                                                                                                                                                                                                             Conservative
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32
37
56
322 AA;
                                                                                                                                                               Query Match
Best Local Similarity
Matches 205; Conserv
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SEQUENCE FROM N.A.
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DISULFID
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P36907;
                                                        DISULFID
                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             199 YGPAGRAIGYDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTARDSA 258
                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 AEQCGSQAGGAVCPNGLCCSKFGFCGSTDPYCGDGCQSQCKSSPTPTIPTPSTGGGDVGR 82
                                                                                                                                    SMART; SM00270; ChtBD1; 1...
PROSITE; PS00026; CHTIN_BINDING; 1.
PROSITE; PS00773; CHTINASE_19_1; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLSF 316
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                                                                                                                                                                                                                                            (BY SIMILARITY).
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BY SIMILARITY.
BY SIMILARITY.
TO 7EDEC8C1AECC3435 CRC64;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                      55;
                                                                                                                                                                                                                                                                                                                                                                                           27 AEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGC-
                                                                                                                                                                                                                                                                                                                                         63.9%; Score 1145.5; DB 67.8%; Pred. No. 1.2e-80; live 32; Mismatches 55
                                                                                                                                                                                                                BY SIMILARITY.
ENDOCHITINASE.
CHITIN-BINDING (
send an email to license@isb-sib.ch).
                                              InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Ffam; PF00187; Chitin_binding; 1.
Ffam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHTINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000509; Chitin_bind; 1.
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                                                                                                                                                                                                            23
320
64
41
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54
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8
                       EMBL; X63899; CAA45359.1;
HSSP; P02877; 1HEV.
                                                                                                                                                                                                                                                                                                                                                                   Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                   Multigene family.
SIGNAL
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Job time: 916 sec
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DISULFID
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 Qγ
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

Мау Run on:

3, 2002, 18:46:59 ; Search time 157.87 Seconds (without alignments) 299.271 Million cell updates/sec

US-09-534-229C-2 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

473505 Total number of hits satisfying chosen parameters: 473505 seqs, 146272329 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SPTREMBL_17:* Database

sp_invertebrate:*
sp_mammal:*
sp_mhc:* sp_virus:*
sp_vertebrate:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_organelle:* sp_rodent:* sp_phage:* sp_human:* 55: 77: 70: 110: 110: 14:::: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_unclassified:*

SUMMARIES

Description	ale za za za zeza zeza zeza zeza zeza ze	V4000/ Oryza sativ
Д	Q9FRV1 Q42294 Q9SQL3 Q9SQL3 Q9AXR9 Q42839 Q42839 Q42934 Q42936 Q4293777 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q42995 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q4295 Q42	
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Query Match	4444 4444 4008 4008 4008 4008 4008 4008	
Score	1336.5 1326.5 136.5 136.5 136.5 126.5 127.5 127.2 127.2 127.2 127.2 127.2 121.3 121.3 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9 111.9	
esult No.	100 H	

09m7g9 arabis glab 09m7g7 arabis glab P94084 medicago sa 094084 medicago sa 094180 nicotiana t 042428 castanea sa 09m7h0 arabis fecu 09sxj3 arabidopsis 09sxj3 arabidopsis 09sxj3 arabidopsis 09sxj3 arabidopsis 09m7f4 arabis pari 09m7f4 arabis pari 09m7f4 arabis pari 09m7f4 arabis sari 09m7f4 arabis ori 09m7f4 arabis lign	
Q9M7G9 Q9M7G9 Q9M7G7 Q4L1B0 Q4L1B0 Q4L1B0 Q9M7H0 Q9SM7H5 Q9SM7H5 Q9M7F4 Q9SM7H6 Q9M7F4 Q9SM7H2 Q9M7H2 Q9M7H2 Q9M7H2 Q9M7H4 Q9M7G1 Q9M7G1 Q9M7G1 Q9M7G1 Q9M7G1 Q9M7G1	
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1170.5 1168 1168 1160.5 1157 1157 1157 1158 1159 1151 1150 1149 1149 1149 1149 1149 1149 1149 114	
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ALIGNMENTS

push dated 69 CGG------GGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFP 116 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Secale. Gaps 9 ATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTG 68 14; Length 321; A Chnuma T. Yamagami T., Ishiguro M.;

"Cloning and Sequencing of the Rye Seed Chitinase.";

"Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB051578; BAB18519:1.

"InterPro: IPR001022; Chitin bind.

"InterPro: IPR001022; Chitin bind.

"Pfam: PF00187; Chitin bind.

"Pfam: PF00187; CHITINBINING.

"ProDom: PD000574; Glyco_hydro_19; 1.

"PRINTS; PR00451; CHITINBINING.

"ProDom: PD000679; Chitin bind; 1. Indels 321 AA; 33641 MW; 76E5902BBC337C8E CRC64; Last sequence update)
Last annotation update) 74.4%; Score 1334; DB 10; 74.4%; Pred. No. 2.2e-112; tive 26; Mismatches 42; 321 AA. Created) SMART; SM00270; ChtBD1; 1.
PROSITE; PS00026; CHITIN_BINDING; 1. PRT; 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-JUN-2001 (TrEMBLrel. 17, Conservative PRELIMINARY; Secale cereale (Rye) Query Match Best Local Similarity Matches 238; Conserv SEQUENCE FROM N.A. SEED CHITINASE-A. NCBI_TaxID=4550; Chitin-binding SEQUENCE 321 Q9FRV1; Q9FRV1 RESULT Q9FRV1 δŏ q Qγ

DYCGPRCQSQCTGCG------GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDA 107

|:|| |||||:||| |DFCGDGCQSQCGGPTPTPTPPSPSDGVGSIVPRDLFBRLLLHRNDGACPARGFYTYEA

61 108

FLAAAGAFPAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSP

167 180 227 228 AIWFWMTTQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVA 287

DRIGETKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323

288

168 PSYCDQSADWPCAPGKQYYGRGPIQLTHNYNYGPAGRALGVDLLNNPDLVATDPTVAFKT

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117 AFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                               236
                                                                                                                                                                                                                         STRAIN-JAPONICA, CV. NIPPONBARE;
MEDLINE=94049667; PubMed=7901749;
Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLRel. 01, Last sequence update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1.4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                           177 WPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQ
                                                                                                                                               Tof rice chitinase genes."

Tof rice chitinase genes."

LOTARATYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-CATALYTIC ACTIVITY: HYDROLYSIS OF CHITIN.

REMBL, X56787; CAA401071; "

REMBL, X66787; CHITINBINDG, 1

REMBL, RE
                                                                                                                                                                                                    SNKPSCHDVIIGLWTPIARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 642F13E3928CA7BE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                    340 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   01, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                          297 CDIFGIGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                   35586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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01-NOV-1996 (TrEMBLrel.
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Last sequence update) Last annotation update)

Created) PRT;

(TrEMBLrel, 13, C) (TrEMBLrel, 13, I. (TrEMBLrel, 17, I.

01-MAY-2000 (01-MAY-2000 (01-JUN-2001 (

320 AA.

PRELIMINARY;

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Ξ,
                                         Poa pratensis (Kentucky bluegrass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----GGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTG 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
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                                                                                                                                                                                                           L Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000966; ARF046454.1; ---
HSSP; PA3931, 2BAA.

R InterPro: IPR00102; Chitin_bind.

R InterPro: IPR00102; Chitin_bind.

R Pfam; PF00182; Glycc_hydro_19.

R Pfam; PF00182; Glycc_hydro_19; 1.

R PRINTS; PR00451, CHITINIBINDG.

R ProDom; PD000609; Chitin_bind; 1.

R PROSITE; PS000726; CHITINASE_19; 1.

R PROSITE; PS00774; CHITINASE_19; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.5%; Score 1317.5; DB 10;
72.6%; Pred. No. 6.7e-111;
Live 33; Mismatches 44; In
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                                                                                                                                                                       SEQUENCE FROM N.A.
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Matches 228; Conserv
                                                                                                                                  NCBI_TaxID=4545;
                                                                                                                                                                                                STRAIN-GLADE;
CHITINASE.
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Gaps

17;

53; Indels

DB 10; Length 340;

74.0%; Score 1326.5; DB 10 70.9%; Pred. No. 1.1e-111; tive 29; Mismatches 53;

Local Similarity 70.9

Best_Loca Matches

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Query Match

1 MSTLRARCATA-----VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTS 55

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Lajoie G.;
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Q42839;
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Matches
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AC Q4
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KQYYGRGPIQLTHNYNYGPAGRAIGVDLINNPDLVATDPTVAFKTAIWFWMTTQSNKPSC 242
                       (1,4-BETA-POLY-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 GGGGGG------VASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFP 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                117 AFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSAD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPCAPGKQYYGRGPIQLTHNYNYGPAGRALGVDLLNNPDLVATDPTVAEKTALWFWTTQ 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Wkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
Yun C.H., Kim J.K., Park Y.H.,
Yun C.H., Kim J.K., Park Y.H.,
Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.
-!-CATALYIIC ACTIVITY: HYDROLYSIS OF THE 1.4-BETA-LINKAGES OF EMBL, 137289, AAAS1377.1;
Mendel, 26; Orysa; Chial, 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.9%; Score 1306.5; DB 10; Length 333; 70.6%; Pred. No. 6.9e-110; Live 35; Mismatches 48; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E2B65D4155B8C73D CRC64;
                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINNSE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycosidase; Hydrolase; Signal.
                                                                                                                                                                                                                                                                                                                         333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mendel, 26, Orysa; Chial; 26, InterPro; IPR001002; Chitin_bind. InterPro; IPR001002; Chitin_bind. InterPro; IPR001705; Glyco_hydro_19. Pfam; PF00187; Chitin_binding; 1. PR1018; PR00182; Glyco_hydro_19; PR0Dom; PR000574; CHITINBIADNG; ProDom; PD000609; Chitin_bind; 1. PROSITE; PS00773; CHITINASE 19_1; PROSITE; PS00774; CHITINASE 19_2; 1. PROSITE; PS00774; CHITINASE 19_2; 1. PROSITE; PS000786; CHITIN_BINDING; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PÔTENTIAL.
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                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                           305 SYGNNLDCYSQRPF 318
                                                                                                                                                                303 GYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          333 AA;
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les 230; Conserv
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Wiseman S.B.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 LDTRKREVAAFFGQISHETIGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGK 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 DVITGLWIPTARDSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRXCDIFGIG 303
                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chitinase genes responsive to cold encode antifreeze proteins winter cereals.", Plant Physiol. 124:1251-1264(2000).
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8
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                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
31.7 KDA CLASS I ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20532799, Pubmed=11080301,
Yeh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wis
Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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BA685E1DB7A58E63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72.2%; Score 1294; DB 10; 71.6%; Pred. No. 8.7e-109;
                                                                                                                                                                                                                                                    318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Æ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332
                                                                                                                  297 CDIFGIGYGNNLDCYNQLSFNVGLAA 322
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                        20
33636 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 71.6 tes 224; Conservative
                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            304 YGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                 Secale cereale (Rye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
318 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 305 YGHNLDCYNQRPF
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4550;
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72 G------GGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTT 121
                                                                                                                        Triticum aestivum (Wheat):
Exkaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae, Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGDGRVADRIGFYKRYCDLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 GDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GKQYYGRGPIQLIHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CHDVITGLWTPTARDSAAGRVPGYGVITNVINGIECGMGQNDKVADRIGFYKRYCDIFG
                                                                                                                                                                                                                                          STRAIN-CY. CHINESE SPRING;
L STRAIN-CY. CHINESE SPRING;
L Plant Sci. 103:177-187(1994).
R REMED: X76041; CAA53626.1; -
R REMED: X76041; CAA53626.1; -
R RASP; P23951; ZBAA.
R Mendel: 1463; Triaes Chial; 1463.
R InterPro: IPR001002; Chitin_bind.
R InterPro: IPR001002; Chitin_bind.
R Pfan, PP00187; chitin_binding: 1.
R Pfan; PP00187; chitin_binding: 1.
R PRING: PR00187; chitin_binding: 1.
R PRING: PR000574; Glyco_hydro_19; 1.
R PRING: PR000574; Glyco_hydro_19; 1.
R PRODOM: PD00069; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
ENDOCHITINASE.
F258D9DD88F65E0E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
3.2.1.14).
             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ENDOCHITINASE PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.6%; Score 1283; DB 10;
70.5%; Pred. No. 8.6e-108;
iive 34; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00270; ChtBD1; 1.
PROSITE; PS00774; CHITINASE_19_2;
PROSITE; PS00026; CHITIN_BINDING;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33602 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLEEL. 01, C3
01-NOV-1996 (TrEMBLEEL. 01, L6
01-JUN-2001 (TrEMBLEEL. 17, L6
ENDOCHTINASE PRECURSOR (EC 3.
CHIAL OR CHT-3.
Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            305 VTYGDNLDCYNQRPF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      302 IGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chitin-binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 3
320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                          Triticeae; Triti
NCBI_TaxID=4565;
                                                                                                      CHIA1 OR CHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sim
les 222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q42994
Q42994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ထ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 CG-----GGGGGVASIVSRDLFERFILLFRN---DAACLARGFYTYDAFLAAAGAFPAFG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 TTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGFFSWGYCFKQEQGSPPSYCDQSADWPC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240 PSCHDVITGIMTPIARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-NON-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE (PC 3.2.1.14) (CHITODEXTRINASE) (1,4 SETA-POLY-N-CHITAL OR CHIT3.
GHAL OR CHIT3.
GHAL OR CHIT3.
FORGeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; NTILicae, Hordeum.
NCBL_TAXID=4513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11 AVLAVVLAAAAVTP--ATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mundy J. M. Telentification of an enhancer/silencer sequence directing the aleurone-specific expression of a barley chitinase gene.";

Li CATALYIC ACTIVIT: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLOCSAMINE POLYMERS OF CHITIN.

EMBL: 134211; AAA56787.1; -

REMBL: 134211; AAA56787.1; -

REMBL: 1565; MOUVUChial; 1565.

InterPro: 1PRO01002; Chitin_bind.

R InterPro: 1PRO01002; Chitin_bind.

R Fam: PRO0187; Chitin_bind.

Probom; PRO0187; Chitin_bind; 1.

PRODOM; PRO0574; CHITINASE_19; 1.

R PROSTIE; PS00773; CHITINASE_19; 1.

PROSTIE; PS00773; CHITINASE_19; 1.

PROSTIE; PS00773; CHITINASE_19; 1.

RR PROSTIE; PS00774; CHITINASE_19; 1.

RR PROSTIE; PS00773; CHITINASE_19; 1.

RR CHITIN_DAIDING; Glycolase; Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 332;
                                                                                                                                                                                                                                                                                                                                Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Ralkhel N.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.8%; Score 1287.5; DB 1071.0%; Pred. No. 3.5e-108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 FGIGYGNNLDCYNQLSFNVGLAAQ 323
                                                                                                                                                                                                                                                                                                            MEDLINE=95078949; PubMed=7987416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         305 LGVGYGGNLDCYNQRPFVEGLLIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 71.0 nes 230; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          TISSUE=SEED;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q41539
Q41539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
Q41539
ID Q4:
AC Q4:
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1;

Gaps

64

124 181 184 241 301 304

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g $\delta \chi$ qq $\delta \Delta$ qq

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56 DYCGPRCQSQCTGCG-----GGGGGVASIVSRDLFERFILHRNDAACLARGFYTYDAFL 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P SEQUENCE FROM N.A.

P SEQUENCE FROM N.A.

STRAIN-IR58; IISSUB-LEAR;
A nuratha C.S., Mew T., Muthukrishnan S.;
L. CATALVITS: TO the EMBL/GenBank/DDBJ databases.

L. CATALVITC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-C.
ACETYL-D-GLUGOSAMINE POLYMERS OF CHITIN,
RELL U02266; AAA18585.1; -1.

RELL U02266; AAA18585.1; -1.

RESP: P23951; 2BAA.
RISSP; P23951; 2BAA.
RISSP; P23951; 2BAA.
RISSP; P23951; 2BAA.
RISSP; PRO01002; Chitin, bind.
RICHEPRO: IPRO0175; Chitin, bind.
RETORN: PRO0187; Chitin, bind.
RETORN: PRO0187; Chitin, bind.
RETORN: PRO0187; Chitin, bind.
RETORN: PRO0187; CHITINBINDNG.
RETORN: PRO0050; CHITIN, BIND, 1.
RETORN: PRO0187; CHITIN, BIND, 1.
RETORN: PROSITE; PS00026; CHITIN, BIND, 1.
RETORN: PROSITE; PS00026; CHITIN, BINDING; 1.
RETORN: PROSITE; PS00026; CHITIN, 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea.
NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AAAGAFPAFGTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 WFWMTPQGNKPSSHDVVTGRWAP-RRDVAAGRA-GYGVITNIVNGGLECGDGPDDRVANR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSTLRARCATA ---- VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSTPRAAASLAKKAALVALAVLAAALATAACAEQCGAQAGGARCPNCLCCSRWGWCGSTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           230 WEWMITQSNKPSCHDVITGLWIPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 335;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47C5FC04D29573C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OI-AUG-1998 (TrEMBLrel. 07, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update) ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           71.0%; Score 1272; DB 10; 70.1%; Pred. No. 8.9e-107; iive 27; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   290 IGFYKRYCDIFGIGYGNNLDCYNQLSFN----VGLAAQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35166 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Persea americana (Avocado)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-1997 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 237; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                  NCBI_TaxID=4530;
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SEQUENCE
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P93680;
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P93680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 LDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQE-QGSPPSYCDQSADWPCAPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 -----GGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGD 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-2001 (TrEMBLrel. 17, Last sequence update)
01-TON-2001 (TrEMBLrel. 17, Last annotation update)
01-TON-2001 (TREMBLREL. 17, Last annotation update)
CHITINASE PRECTESOR (EG. 3.2.1.14) (CHITINASE) (1,4-BETA-POLY
CHITINASE SALIVA (Rice).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 KQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSC
         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryzea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOCHITINASE.
D7331BF4A6B592E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  335 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 AA; 33681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 72.0
Matches 224; Conservative
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                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                 STRAIN=NIPPONBARE;
                                                                                                       NCBI_TaxID=4530;
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042970;
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STRAIN=NIPPONBARE;
MEDLINE-94049667; PubMed=7901749;
Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 PTPVTPTPSGGGGVSSLVSQSLFEQMLLHRNDPSCQANGFYTXKAFIAAANSFAGFGTTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         123 DLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 KQYYGRGPIQLIHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWWTTQSNKPSC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 HDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDK--VADRIGFYKRYCDIF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            042993; 04296; Carberrance, Created)
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-0NOV-1996 (TrEMBLrel. 17, Last annotation update)
01-JUN-2001 (TrEMBLRel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                    6 VVAILVAAFAVS-AHAEQCGSQAGGATCPNCLCCSKFGFCGNTSDYCGTGCQSQCNGCSG
                                                                                                                                                                                                                                                                                                                            Length 340;
                                                                                                                                                                                                                                                                  340 AA; 36011 MW; 3613D7059A871E94 CRC64;
                                                                                                                                                                                                                                                                                                                          70.0%; Score 1254; DB 10;
69.3%; Pred. No. 3.8e-105;
iive 40; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 323 AA.
                 Interpro; IPR001002; Chitin_bind.
Interpro; IPR0010726; Glyco_hydro_19.
Ffam; PF00187; Chitin_binding; 1.
Ffam; PF00182; Glyco_hydro_19; 1.
FRINES; PR00451; CHTINBIADNG.
Frobom; PD000574; Glyco_hydro_19; 1.
FROSTIE; PS00773; CHITINASE_19_1; PROSTIE; PS00773; CHITINASE_19_1; PROSTIE; PS00774; CHITINASE_19_2; 1.
FROSTIE; PS0076; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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Mol. Gen. Genet. 241:1-10(1993).
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Plant Sci. 76:211-218(1991).
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                                                                                                                                                                                                                                                                                                                                                Similarity
  HSSP; P23951; 2BAA
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                                                                                                                                                                                                                                            Chitin-binding.
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Best Local Simi
Matches 219;
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Q42993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     191 IQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLW 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 TPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poa pratensis (Kentucky bluegrass).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsída, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 VLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGFTSDYCGFRCQSQCTG-CG 70
                 Sowka S., Hsieh L., Krebitz M., Akasawa A., Martin B., Starrett D., Peterbauer C., Scheiner O., Breiteneder H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; Z78202; CAB01591.1; -.
RMSP; POSS77; HEV.
Mendel; 14766, Perae-Chial;14766.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00176; Glyco_hydro_19.
Ffam; PF00187; chitin_binding; I.
Ream; PF00182; Glyco_hydro_19; I.
R PRIVES; RR00451; CHITINBINDNG.
R PCDDOW; PD000609; Chitin_bind; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 VAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                               643B20589E062E61 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.1%; Score 1256; DB 10;
69.8%; Pred. No. 2.4e-105;
live 36; Mismatches 55;
                                                                                                                                                                                                                                                              340 AA.
                                                                                                                                                                                                                                                                                                                                                                                                              ENDOCHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
STRAIN-CV. HASS; TISSUE-MESOCARP,
                                                                                                                                                                                                                                                                                                                                                                                                                             34586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAX-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 220; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 YNQLSFNVG---LAA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 YNQRSFGVSTNPLAA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                   26 3
325 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Submitted (APR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-GLADE;
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                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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Q9SQL4
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Matches 212;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 SCGGGGPTPPSGGGGSGVASIVSRSLFDQMLLHRNDAACPAKNFYTYDAFVAAANAFPSF 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 GTTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQ----GSPPSYCDQS 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     235 TQSNKPSCHDVITGLMTPTARDSAAGRVFGYGVIINVINGGIECCMGQNDKVADRIGFYK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 POSPKPSCHAVMTGQWTPNGNDQAAGRVPGYGVVTNIINGGVECGHGADSRVADRIGFYK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATAVLAVVLAAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTG 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

R EMBL, D1621; BAA03749.1, -.

R EMBL, X65063; CAA39535.1, -.

R HSSP; P23951; 2BA.

R HSSP; P23951; 2BA.

R Medel: 14776; Orysa: Chial.14776

R InterPro; IPR001002; Chial.n_bind.

R InterPro; IPR001002; Chial.n_bind.

R Ffam; PP00187; Chial.n_bind.ng; 1.

R Ffam; PP00187; Chial.n_bind.ng; 1.

R PRINTS; PR00451; CHITINNON.

R PRODOM; PD000059; Chial.n.

R PROSITE; PS00704; Chial.n.

R PROSITE; PS00774; CHITINASE 19-1; 1.

R PROSITE; PS00774; CHITINASE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Allium sativum (garlic).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales, Alliaceae,
Allium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.1%; Score 1238.5; DB 10; Length 323; 69.3%; Pred. No. 8.9e-104; Live 31; Mismatches 51; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                 ENDOCHITINASE,
: 1C85B6227A33EB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Van Damme E.J., Willems P., Peumans W.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL, M94105; AAA32641.1;
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TTEMBLIEL. 01, Created)
01-NOV-1996 (TTEMBLIEL. 01, Last sequence update)
01-JUN-2001 (TTEMBLIEL. 17, Last annotation update)
CHITINASE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                295 RYCDIFGIGYGNNLDCYNQLSFN 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          300 RYCDMLGVSYGANLDCYNQRPFN 322
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33764 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      705; Allsa; Chial; 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               323 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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SEQUENCE FROM N.A.
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Best Local Simil
Matches 224;
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SEQUENCE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 APGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMTTQSNK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 PSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGONDKVADRIGFYKRYCDI 299
                                                                                                                                                                                                                                                                                                                                                                 12 VLAVVLAAAAVTPATABQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGFRCQSQCTGCGG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGDLDTRKREVAAFFGQTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allium sativum (Garlic).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;
                                                                                                                                                                                                                                                                                                                                            Indels 12;
                                                                                                                                                                                                                                                                                                               Length 318;
                                                                                                                                                                                                                     POTENTIAL.
CHITINASE.
; 097C3DBD772468D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Van Damme E.J., Willems P., Peumans W.;
Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
EMBL, M94106, AAA32640.1;
EMBL, M94106, AAA32640.1;
EMBL, P23951, 2BAA.
Mendel; 704; Allsa;Chial;704.
Mendel: 704; PR001002; Chitin_bind.
InterPro; IPR00702; Chitin_bind.
InterPro; IPR007026; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19;
PRINTS; PR00451; CHITINBINDNG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03.0776;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                     67.7%; Score 1213; DB 10;
66.9%; Pred. No. 1.7e-101;
htive 39; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 AA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Chitin_binding; Signal.
NON_TER.
SIGNAL.
1 17 POTENTIAL.
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                                                                                                                                                                                                                                    18 318 C
318 AA; 33175 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 FGIGYGNNLDCYNQLSF 316
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                        18
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Search completed: May
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECUSSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLX-N-ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
CHIAI OR RC24.
                                                                                                                                                                                                                                                                                                                                                                                                                                  76 VASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAFGTTGDLDTRKREVAAFF 135
                                                                                                                                                                                                                                                                                                                                                          GOTSHETTGGWPTAPDGPFSWGYCFKQEQGSPPSYCDQSADWPCAPGKQYYGRGPIQLTH 195
                                                                                                                                                                                                                                                                                                                                                                          NYNYGPAGRAIGVDILNNPDLVATDPTVAFKTAIWFWMTTQSNKPSCHDVITGLWTPTAR 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSAAGRVPGYGVIINVINGGIECGMGQNDKVADRIGFYKRYCDIFGIGYGNNLDCYNQLS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                      16 VLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCTGCGGGGGG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1]
SEOUBNICE FROM N.A.
STRAIN=1R36; TISSUE=LEAF;
MEDLINE=96189226; PubMed=9605293;
Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
"Regulation, expression and function of a new basic chitinase gene"
"Regulation, expression and function of a new basic chitinase gene"
"Regulation, expression and function of a new basic chitinase gene"
"Regulation, expression and function of a new basic chitinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; Liliopsida, Poales; Poaceae;
Ehrhartoidese; Oryzea, Oryza.
                                                                                                                                                                                                                                                                                                                   62 VASIISSSLFNQMLLHRNDAACPANGFYTIDAFIAAANSFSGFGTTGDTDKRELAAFF
                                                                                                                                                                                                                                                        rice (oryza sativa L.).,
Plant Mol. Biol. 30:387-401(1996).
-!-CATALYIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF I
ACETYL-D-GLGCOSAMINE POLYMERS OF CHITIN.
BERBI, X87109; CAA60590.1;
HSSP; P23951; ZBAA.
Mendel, 1634; Orysa,Chial;1634.
InterPro; IPRO01002; Chitin_bind.
InterPro; IPRO0102; Chitin_bind.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00187; chitin_binding; 1.
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                                                                                                                                                                                Length 302;
                                                                                                                                                                                                           Indels
                                                                                                                                 D0687D330BFFD75F CRC64;
                                                                                                                                                                             67.2%; Score 1204; DB 10;
69.4%; Pred. No. 1.1e-100;
live 33; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     322 AA.
                                                                                                      POTENTIAL.
CHITINASE.
Probom, PD000574; Glyco_hydro_19; 1.
SMART; SM00270; ChtbDl; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00074; CHITINASE_19_2; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
Chitin-binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                   31728 MW;
                                                                                                                                                                             Query Match 67.2%,
Best Local Similarity 69.4%,
Matches 209; Conservative
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                                                                                                                    302
                                                                                                                                 302 AA;
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SIGNAL
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68 ------GCGGGGGGVASIVSRDLFERFLLHRNDAACLARGFYTYDAFLAAAGAFPAF 118
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                     9 ATAVLAVVLAAAAVTPATAEQCGSQAGGAKCADCLCCSQFGFCGTTSDYCGPRCQSQCT- 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 ADWPCAPGKQYYGRGPIQLTHNYNYGPAGRAIGVDLLNNPDLVATDPTVAFKTAIWFWMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TQSNKPSCHDVITGLWTPTARDSAAGRVPGYGVITNVINGGIECGMGQNDKVADRIGFYK
                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                             Length 322;
                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                 SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;
                                                                                                                                                                                                                         Query Match 66.5%; Score 1192; DB 10; Best Local Similarity 67.2%; Pred. No. 1.4e-99; Matches 217; Conservative 30; Mismatches 56;
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000509; Chitin_bind; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
PROLITE; PS00026; CHITIN_BINDING; 1.
SIGNAL
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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3, 2002, 18:30:30; Search time 117.39 Seconds (without alignments) 201.290 Million cell updates/sec May Run on:

US-09-534-229C-3 Perfect score: Title:

1765 1 MRGVVVVAMLAAAFAVSAHA......DLLGVSYGDNLDCYNQRPFA 319 Sednence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 Total number of hits satisfying chosen parameters:

522463 seqs, 74073290 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08 Maximum Match 1008 Listing first 45 summaries

Database :

SIDS2/goddata/geneseq/geneseqp/AA1980.DAT:*
SIDS2/gogdata/geneseqp/AA1981.DAT:*
SIDS2/gogdata/geneseqp/AA1981.DAT:*
SIDS2/gogdata/geneseqp/AA1983.DAT:*
SIDS2/gogdata/geneseqp/AA1983.DAT:*
SIDS2/gogdata/geneseqp/AA1985.DAT:*
SIDS2/gogdata/geneseqp/AA1985.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp/AA1993.DAT:* /SIDS2/gcgdata/geneseg/genesegp/AA1999.DAT:*/SIDS2/gcgdata/geneseg/genesegp/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp/AA2001.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1995.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1996.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:* /SIDS2/gcgdata/geneseq/geneseqp/AA1998.DAT:* A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Wheat chitinase or	Rye chitinase-like	Rye chitinase-like	RCH10 chitinase pr	Rice chitinase. 0	Wheat chitinase pr	Amino acid sequenc	Basic chitinase 48	Chitinase encoded	Tobacco intracellu	Nicotiana sp. intr
SUMMARIES	AAB11489	AAW98079	AAW98080	AAR29019	AAR67969	AAB11488	AAB67444	AAR15841	AAR11305	AAR13275	AAW31297
DB	22	20	20	13	16	22	22	12	12	12	18
% Query Match Length DB	319	318	298	336	336	323	336	329	331	324	324
% Query Match	100.0	95.7	90.2	73.7	73.7	73.3	73.2	72.0	71.2	70.9	70.9
Score	1765	1688.5	1597.5	1301.5	1301.5	1294.5	1291.5	1270.5	1256.5	1252	1252
Result No.	-	7	3	7	Ŋ	9	7	80	σ	10	11

AABO7513 AARS0822 AARS0802 AAW00186 AAW24554 AAR24554 AAR2455577 AAR52577 AAR52577 AAR52577 AAR52814 AAW90169 AAR13274 AAR13274 AAR13274 AAR13274 AAR13274 AAR13274 AAR13274 AAR13274 AAR18905 AAR18903 AAR18903 AAR18903 AAR18903 AAR18903 AAR18904 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914 AAR18914	Amino acid sequenc Sequence of endoch Endochitinase prec American elm chiti Chitinase. Cucurb Sequence of a 302	Chitinase G. Hord Floral organ-speci Banana ripening fr	C. ensiformis chit Petunia extracellu Petunia hybrida ex	Amino acid sequence A maize chitinase Sugar beet chitina		Tobacco endochitin A maize chitinase	A maize chitinase Rye chitinase-like	Mye difference from Wheat childrase pr Protein encoded by	Wild tomato endoch	A maize chitinase	Amino acid sequenc A maize chitinase	Amino acid sequenc		A maize chitinase Arabidopsis thalia
		52577 64776 05844	90169 13274 31296	07512 18905 28150	28415	76714 18902	18903 98081	11487 28788	76713	18894	18906 18904	18936	28147 28145	1889 5365
	21 13 15 17 18	119	20 12 18	21 21 21	21	16 21	20 20	222	100	27	27	12,	5 T	21
777777777777777777777777777777777777777	328 328 329 292	266 328 2466	243 254 254	254 284 294	272	253 259	252	256	250	281	155	271	264	261 813
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8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	1252 1202.5 1202.5 1192.5 1156	1125 1066 1003	927 805.5 805.5	805.5	786.5	777.5	769.5	734	710.5	618	612.5	- 0	ת	515.5
1252 70.9 324 92.5 68.1 328 92.5 67.6 317 92.5 67.6 317 92.5 67.6 317 92.5 67.6 317 92.7 66.4 246 92.7 266.8 246 92.7 266.8 246 92.7 266.8 246 92.7 266.8 246 92.7 45.6 254 93.7 44.0 255 93.7 44.0 253 93.7 44.0 253 93.8 44.6 272 93.8 44.6 272 93.8 44.0 253 93.8 44.0 253 94.5 46.3 253 94.5 46.3 253 95.5 34.1 271 97.5 34.1 271 97.5 264 97.5 264	11111 211111 10111111111111111111111111	18 19 20	21 22 23	24 25 25	224	30 30 30	337	3.4 4.4	36	, eo	39 40	41	4 4 2 6	44 45
1252 70.9 324 1202.5 68.1 328 1192.5 68.1 328 113.5 66.5 5 203 113.2 66.4 2 203 1003 66.4 2 203 1005 66.4 2 203 1005 66.4 2 203 1005 56.8 24.6 66.4 2 203 1005 5 45.6 224 805.5 45.6 224 805.5 44.6 225 777.5 44.0 225 777.5 44.0 225 777.5 74.0 44.0 225 777.5 74.0 225														

ALIGNMENTS

Wheat, chitinase, low temperature expression; hardened; plant, snow mould resistance; psychophilic plant pathogen; spring wheat. Wheat chitinase protein homologous to spring wheat chitinase. AAB11489 standard; protein; 319 AA. 99JP-0081694. 99JP-0081694. (first entry) Triticum aestivum. JP2000270866-A. 25-MAR-1999; 25-MAR-1999; 03-OCT-2000. 02-MAR-2001 AAB11489; RESULT AAB11489

(HOKK-) HOKKAIDO NOGYO SHIKENBACHO.

WPI; 2001-027417/04.

New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes $\,$

Claim 7; Fig 3; 11pp; Japanese.

This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression

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chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat P1173438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant pathogenic microbes.
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                                                                                                                                                                                                                   241 KPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCD 300
                                                                                                                                                 ATTGSIDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTFSSQWP 180
                                                                                                                                      GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                                 Gaps
                                                                                                     1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                         CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy.
                                                                                                                                                                                                          CAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1..20
/note= "signal peptide"
21..318
/note= "mature protein, also claimed in Claim 10"
                                                                                     :0
                                                                   Length 319;
                                                                                     Indels
                                                                    Score 1765; DB 22;
Pred. No. 1.1e-137;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         Rye chitinase-like protein CHT9 preprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                                                                                                                      AAW98079 standard; Protein; 318
                                                                    100.0%; Silarity 100.0%; P
                                                                                                                                                                                                                                                                            LLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                      97US-0903B72.
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ICEB-) ICE BIOTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-153795/13.
N-PSDB; AAX24889.
                                                                    Query Match
Best Local Similarity
Matches 319; Conserv
                                           319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Secale cereale.
                                                                                                                                                                                                                                                                                                                                                                       21-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-FEB-1999
                                                                                                                                                                                                                                                                                                                                                       AAW98079;
                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
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The present sequence is winter rye (Secale cereal L. cv. Muskateer)
CHT9 preprotein. The mature protein, which is also claimed, is a
Chitimase-like protein that has chitimase (antifungal) and
antifreeze activities. CHT9 cDNA (see AAXA889) was obtained by
isolating mRNA from rye plants grown at low temperatures in the
abstract of pathogens or other stresses, i.e. under conditions when
only chitimases with antifreeze activity would be expressed. CHT9
and CHT46 (see AAW88081-82) have been cloned and expressed in
bacterial and yeast (Pichia) systems and in Arabidopsis thaliana.
The chitimase-like antifreeze proteins can be used: to increase
freezing tolerance of plants and microorganisms; to increase field
survival of plants, animals and microorganisms exposed to sub-zero
temperatures; to inhibit ice recrystallisation in biological
materials or foods; for cryopreservation and hypotherature
of cells, embryos, tissues etc. (particularly human platelets); and
to kill tumour cells. They are also used to inhibit initiation and
properssion of diseases or spoilage caused by to temperature
pathogens (particularly fungi) in plants, frozen foods and any
cryopreserved biological material. The signal peptide can be used
to to direct protein secretion in transgenic organisms or expression
ever and the particularials.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWP 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRGVVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1688.5; DB 20.
Pred. No. 2.1e-131;
9; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW98080 standard; Protein; 298 AA.
                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rye chitinase-like protein CHT9.
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                                                                                                                                    Claim 10; Fig 21a; 118pg;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 AA;
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Best Local Simi
Matches 304;
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ID AAW98
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Tue May

240 agrvpgygvitniingglecgrggdarvadrigfykrycdllgvsygdnldcyngrpfa 298

qq

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New nucleic acid encoding antifreeze polypeptides from plants - particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells etc. and for treating tumours
winter rye, antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xlong F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 10; Fig 21d; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moffatt B,
                                                                                                                                                                                                                                                                                 98WO-CA00745.
                                                                                                                                                                                                                                                                                                                                             97US-0903872.
                                                                                                                                                                                                                                                                                                                                                                                                         (ICEB-) ICE BIOTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffith M, Hew C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-153795/13
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                                                                                                     Secale cereale.
                                                                                                                                                              WO9906565-A2
                                                                                                                                                                                                                                                                                                                                             31-JUL-1997;
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cobtained by isolating mRRA from rup pippinein. CUMA (See AAAAEBUS) was continued by isolating mRRA from rup pippinein curve clear three activity would be expressed. In the absence of pathogens or other stresses, i.e. under conditions in the absence of pathogens or other stresses, i.e. under conditions in the absence of pathogens or other stresses, i.e. under conditions in the absence of pathogens in the respectivity would be expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chiminase like antiffeeze proteins can be used; to increase field survival of plants, animals and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and progression of diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved biological material. Mature CHT9 The present sequence is winter rye (Secale cereal L. cv. Muskateer) CHT9 mature protein. It lacks the 20-amino acid signal peptide of the preprotein (see AAW98079), which is also claimed. Mature CHT is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT9 preprotein cDNA (see AAX24889) was

Sequence

;; 141 SHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQISHNYN 200 201 YGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDV1TGRWSPSGADQA 260 81 IISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVAAFLAQT 140 AGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYNQRPFA 319 Gaps 1 eqcgsqaggatcpnclccskfgfcgstseycgdgcqsqcnrc-ggtpvpvptptgggvss 59 EQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSGGTPVPVPTPSGGGVSS ; ; DB 20; Length 298; 5; Indels 90.5%; Score 1597.5; DB 20 95.0%; Pred. No. 6.3e-124; iive 9; Mismatches 5; Query Match
Best Local Similarity 95.0'
Matches 284; Conservative 180 21 9 120 261 g δ ŏ 셤 δà Q δŽ

4

The sequence given is encoded by the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this protein in mature plants is characteristic. There is a low level of expression in mature leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes. 60 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112 61 srlrrrrpdasgg-----ggsgvasivsrslfdlmllhrndaacpasnfytdafva 112 113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD 171 17; Gaps 1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC 59 /note= "Region conserved between class I and class II chitinases" Promoter; region; rice; chitinase; physical; biological; stress; Length 336; DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level expression in roots leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes. 47; Indels Score 1301.5; DB 13; Pred. No. 1.8e-99; 27; Mismatches Disclosure; Page 33-34; 45pp; English. (SALK) SALK INST BIOLOGICAL STUDIES Location/Qualifiers Æ AAR29019 standard; Protein; 336 73.78; 91US-0704288 Conservative RCH10 chitinase protein. WPI; 1992-415785/50. Similarity 336 AA; N-PSDB; AAQ31407 Zhu Q; Oryza sativa. Query Match Best Local Simi Matches 237; 22-MAY-1991; WO9220807-A 20-APR-1993 26-NOV-1992 Sequence Lamb CJ, AAR29019; Region AAR29019 Db δy g ŏ

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---ggsgvasivsrslfdlmllhrndaacpasnfytydafva 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%; Score 1294.5; 71.0%; Pred. No. 6.6e
                                                                                                                                          IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
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                                                                                                                                                                                                                                                                                                                                                                               99JP-0081694.
                                                                                                                                                                                                                                                                                                                                                            99JP-0081694
                                                                                                                                                                                                                                      (first entry)
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 srlrrrrpdasgg-
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Matches 22
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61
                                                                                                                                                                             RESULT
AAB11488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                        291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The SphI fragment of rice chitinase RCHIO gene (given in AAQ81346) an alfalfa beta-1.3-glucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and Thanatephorus cucumeris fungal infection.
WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                             YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 336;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when
                                                                                                                                                                                                                                             Chitinase; transgenic plant; disease resistance;
crop improvement; tobacco; Nicotiana tabacum; plant defense;
fungus pathogen; Cercospora nicotinae;
Thanatephorus cucumeris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1301.5; DB lb;
Pred. No. 1.8e-99;
----nes 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 31-32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          Zhu Q;
                                                                                                                IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                        (SALK ) SALK INST BIOLOGICAL STUDIES.
                                                                                                                                                                       AA
                                                                                                                                                                    AAR67969 standard; Protein; 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        grown in crops as a food source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                                                                                          EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.7%;
72.3%;
                                                                                                                                                                                                                                                                                                                                                   94WO-US07815.
                                                                                                                                                                                                                                                                                                                                                                     93US-0093372.
                                                                                                                                                                                                                                                                                                                                                                                                          Maher
                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         Lamb CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1995-067090/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAQ81346.
                                                                                                                                                                                                                            Rice chitinase.
                                                                                                                                                                                                                                                                                            Oryza sativa
                                                                                                                                                                                                                                                                                                                                                  15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                     16-JUL-1993;
                                                                                                                                                                                                          13-AUG-1995
                                                                                                                                                                                                                                                                                                              WO9502319-A.
                                                                                                                                                                                                                                                                                                                                 26-JAN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237;
                                                                                                                                                                                                                                                                                                                                                                                                          Dixon RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                        AAR67969;
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Matches
                                              173
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          113
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                                                                                                                                                                                        δλ
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This invention describes novel wheat chitinase genes. The invention also describes a method for the isolation of a low temperature expression chitinase gene in which the mRNA is extracted from a fully hardened autumn wheat P1173438 (of high snow mould resistance). The genes are useful for creating a plant grade, highly resistant to psychophilic plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New low temperature expression chitinase gene for producing a plant grade highly resistant to psychophilic plant pathogenic microbes
                                                                                                                                     YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
                                                                                                                                                                                                              232 WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                           5 VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG
113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wheat, chitinase, low temperature expression; hardened; snow mould resistance; psychophilic plant pathogen; rye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ______ DB 22; L
red. No. 6.6e-99;
Mismatches 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wheat chitinase protein homologous to rye chitinase.
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AAR15841
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                                                                                                                                                      Db
                                                                                                                                                                                ΩŸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a chitinase designated RCHIO. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCHIO protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomonas spp.. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to
                                                                                                                                                                                                                                                                                                                                                                                          Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
                                                                     STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
                           123 dldtrkrevaaffgqtshettggwptapdgpfswgycfkqeqgsppsycdqsadwpcapg
                                                     KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a rice chitinase designated RCH10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           confer desired traits on essentially any plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 45-46; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lamb C,
                                                                                                                                                                                                                                                                           AAB67444 standard; Protein; 336 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-JUL-2000; 2000WO-US20714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0363313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                He Z, Chory J,
                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGC ) UNIV CALIFORNIA
                                                                                                                                                                         SYGDNLDCYNORPF 318
                                                                                                                                                                                                    303 gygnnldcynglsf 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-159858/16.
                                                                                                                                                                                                                                                                                                                                                                                             Disease resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAF54983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                    15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ronald P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                       AAB67444;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (SALK)
                                                                                                                                             243 ]
                                                        185
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                                                                                                                                                                                                                                                            AAB67444
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Gaps

17;

Indels

73.2%; Score 1291.5; DB 22; 71.6%; Pred. No. 1.2e-98; ive 27; Mismatches 49; In-

Conservative

Query Match Best Local Similarity Matches 235; Conserv

Length 336;

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172
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                                                                                                                                                   291
                                                                                                                                                                                                 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                                                                         171
                      9
                                                                                                       :
srlrrrpdasgg-----ggsgvasivsrslfdlmllhrndaacpasnfytydafva
MRGVVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC
                       1 mralavvamvarpflaaavhaeqcgsqaggavcpnclccsqfgwcgstsdycgagcgsqc
                                                                                            113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                        YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
                                                                                                                                                                                   WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA sequence encoding vacuole targetting peptide - esp. signal region of tobacco chitinase or glucanase gene, and derived recombinant DNA, vectors, etc. functional in plants
                                                                                                                                                                                                                                                                                                                                                                                                             Vacuole; targetting; chitinase; glucanase; signal; resistance; pharmaceutical; hormones; expression; secretion; extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= sig_peptide
/note= "used as vacuole targetting peptide"
                                                                                                                                                                                                                                                                                                                                                                                     Basic chitinase 48 from clone lambdaCHN17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 64-68; 81pp; English
                                                                                                                                                                                                                                               IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana tabacum L. c.v. Havana 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= exonl_prod.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= exon2-prod.
200..329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= exon3_prod.
318..329
                                                                                                                                                                                                                                                                                                                   AA
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                                                                                                                                                                                                                                                                                                                   AAR15841 standard; Protein; 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91EP-0810430.
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                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1991-371028/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAQ15147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EP462065-A.
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                                                                                                                                                                                                                                                                                                                                          AAR15841;
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Region
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EP440304-A.
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                                                                                                                                                                          Sequence
                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                         126
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                                                                                                                                                                                                                                                                            PVPVPTPSGGG-VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
                                                                                                                                                                                                                                   DVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
Attachment of the signal peptide ensures occlusion of expressed prod. in the vacuole while elimination of the signal peptide from a sequence normally contg. it ensures that the expressed product is secreted into the extracellular space, rather than retained in protects the plant, e.g. resistance to pathogens, herbicides, insecticides, blocides, environmental stress, etc.; leads to pharmaceuticals such as hormones or immunommodulators. See also AAQ15146-50 and AAQ15330-35.
                                                                                                                                                                                            8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG~CQSQCNGCSGGT
                                                                                                                                                                                                                                                               TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNOERGATSDYCTPSSOWPCAPGK
                                                                                                                                                                                                                                                                                                     KYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH
                                                                                                                                          Length 329;
                                                                                                                                                              5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New DNA regulatory sequence from new tobacco chitinase gene
                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant chitinase; transgenic plants; pathogen resistance
                                                                                                                                          DB 12;
                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chitinase encoded by genomic clone lambda CHN17
                                                                                                                                                      Pred. No. 6.4e-97
                                                                                                                                          72.0%; Score 1270.5; 72.8%; Pred. No. 6.4e
                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuhaus J-M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR11305 standard; Protein; 331
                                                                                                                                                             29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89CH-0003334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                   306 YGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                     pgdnldcgnqrsf 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meins F, Shinshi H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1991-088356/13.
N-PSDB; AAQ11093.
                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum.
                                                                                                              329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-SEP-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-1990;
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                                                                                                                                                Best Local Sim
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                                                                                                              Sequence
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      308
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67 PVPVPTPSGGG-VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11 sllfslllsasaeqcgsqaggarcpsglccskfgwcgntndycgpgncqsq---cpggp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSS-QWPCAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
                                                                                                                                     This recombinant tobacco chitinase gene prod. is encoded by a genomic close, lambda CHNI7 which comprises 3 exons and has 5' - and 3' - untranslated regions. A fragment (claimed) from the 5'-untranslated region can be used to increase the ex-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 12; Length 331;
                                                                                                                                                                                                                             pression of foreign genes, in transgenic plants. The fragment is linked to a foreign gene, eg chitinase or glucanase gene via a spacer and is also linked to regulatory sequences. The resultant DNA construct is used to transform plant cells, eg tomato or tobacco, which subsequently produce the gene product at high level.
  of foreign genes in transgeni resistance to pathogens etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intracellular chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30; Mismatches 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%; Score 1256.5; 72.1%; Pred. No. 9.2e
used to increase expression of foreign
plants, partic for improving resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13275 standard; Protein; 324 AA
                                                                                  65pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fungal resistance; phytopathogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tobacco intracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nicotiana tabacum Samsun NN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 72.19
Matches 227; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24..324
/label= i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     304 VSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    || ||||||| ||| || || vspgdnldcgnqrsf 322
                                                                                     page 44;
                                                                                                                                                                                                                                                                                                                                                                                                              See also AAQ11094.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-0CT-1991
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243

307

184 187

5,

67

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324 AA;
  Nicotiana sp.
                                                                                                            19-APR-1993;
                                                                                                                             29-JAN-1991;
                                                                         US5670706-A.
                                                                                           23-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                             Peptide
                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ΩŸ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                                                                                                                                                                                                                        PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                      99
                                                                                                                                                                                                                                                                                                                                        99
                                                                                                                                                                    The sequence from which this amino acid was deduced was isolated from a N.tabacum Chalbrary following screening with a partial tobacco intracellular chitinase clone. The protein sequence appears twice in the specification but in one (not the one given in this file), the Leu codons at positions -23, -21, -15, -12, -11, -8, -7, -6, -5 and plus 16, 52, 65, 137, 176, 177, 182, 195, 228, 242, 266, 274, 286 are translated as Ile.
                                                                                                                                                                                                                                                                                                                              8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                                                                                                          127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK
                                                                                                                                                                                                                                                                                                                                                                                                     187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                           247 VIIGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intracellular chitinase, antifungal, transgenic plant, synergism, beta-1,3-glucanase gene; tobacco.
                                                                                                                                                                                                                                                                                                   8
                                                                                                                 Plants with improved resistance to pathogenic fungi - contains chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                             Roekel JS;
JF;
                                                                                                                                                                                                                                                                                  Length 324;
                                                                                                                                                                                                                                                                                                   Indels
                                                               Van
Bol
                                                                                                                                                                                                                                                                                70.9%; Score 1252; DB 12; 71.8%; Pred. No. 2.1e-95;
                                                                                                                                                                                                                                                                                         2.1e-95;
ches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intracellular chitinase protein.
                                                              Meulenhoff EJ,
Woloshuk CP,
                                                                                                                                                                                                                                                                                          Pred. No. 2.16
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW31297 standard; Protein; 324 AA
                                                              Melchers LS, N
, Vloemans AA,
                                                                                                                                                     Example 4; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                 29;
                                   (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV TE LEIDEN.
                  90NL-0000222
91EP-0200191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gdnldcgngrsf 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDNLDCYNQRPF 318
                                                                                      WPI; 1991-232019/32.
N-PSDB; AAQ12898.
                                                                                                                                                                                                                                    See AAQ12897-Q12900
                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                      324 AA;
                                                                       Sela-Buurlage MB,
                                                              Cornelissen BJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicotiana sp.
30-JAN-1991;
                   30-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-MAR-1998
                                                                                                                                                                                                                                                                                                  Matches 224;
                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW31297
                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                       29
                                                                                                                                                                                                                                                                                                                                                                         69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307
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8
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                                                                                                                                                                                                                                                                                                                                                       \delta \lambda
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                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
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to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes exhibit a synergistic antifungal effect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8 AMLAAARAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence represents an intracellular chitinase which is used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fungus-resistant transgenic plants - containing genes encoding intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                      Cornelissen BJC, Linthorst HJM, Melchers LS; ff EJS, Sela-buurlage MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.9%; Score 1252; DB 18; 71.8%; Pred. No. 2.1e-95; ive 29; Mismatches 51;
                                                                                        "intracellular protein"
                      1..23
/label= signal_peptide
24..324
/note= "intracellular g
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 4; Fig 2; 42pp; English.
                                                                                                                                                                                                                                       93US-0047413
                                                                                                                                                                                                                                                                                  91US-0647831
                                                                                                                                                                                                                                                                                                                                                                                                   Bol JF, ....
Meulenhoff EJS, Sela-burr
AA, Woloshuk CP;
                                                                                                                                                                                                                                                                                                                               (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV LEIDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 71.8
nes 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||||||| ||| |
gdn||dcgngrsf 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-479536/44.
N-PSDB; AAT89952.
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us-09-534-229c-3.rag

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247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                 (SNFI ) SANOFI SA.
(ERAP ) SOC NAT ELF AQUITAINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example; Fig 4; 82pp; French.
                                                                                                                                                                                                                                                                                                                                                                        91WO-FR00607.
                                                                                                                                                                                                                                                                                                                                                                                              90FR-0009460.
                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                   304 gdnldcgnqrsf 315
                                                     307 GDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Grison R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-064950/08.
N-PSDB; AAQ21193.
                                                                                                                                                                                                                                               Tomato and tobacco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               328 AA;
                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1991;
                                                                                                                                                                                                                                                                                                                                                                                             24-JUL-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Simi
Matches 213;
                                                                                                                                                                       16-MAY-1992
                                                                                                                                                                                                                                                                                                                              WO9201792-A.
                                                                                                                                                                                                                                                                                                                                                   06-FEB-1992,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dubois M,
                                                                                                                                                   AAR20822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                           nematode
                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                    AAR20822
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                                                                         QD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungithe recombinant polynuclectides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                                                                                                                                                                                                       New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                           Melchers LS, Meulenhoff EJS, Sela-buurlage MB; oshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 324;
                                                                                                    Chitinase; transgenic plant; beta-1,3-glucanase; antifungal; plant resistance; pathogenic fungi; fungal resistant plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                 Amino acid sequence of an extracellular chitinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1252; DB 21
Pred. No. 2.1e-95;
9; Mismatches 51
                                                                                                                                                                             /note= "signal peptide"
                                                                                                                                                         Location/Qualifiers
                  AAB07513 standard; Protein; 324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 2A-B; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%; Scor
71.8%; Pred
ative 29;
                                                                                                                                                                                                                                                               93US-0047413.
91US-0647831.
                                                                                                                                                                                                                                           97US-0801563
                                                                                                                                                                                                                                                                                                                                       Woloshuk CP,
                                                             (first entry)
                                                                                                                                                                                                                                                                                             (UYLE-) RIJKSUNIV LEIDEN. (MOGE-) MOGEN INT NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-498214/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AA;
                                                                                                                                                                                                                                                                                                                            Cornelissen BJC,
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAA58910
                                                                                                                                                                                                                                                                                                                                       Vloemans AA,
                                                                                                                                    Nicotiana sp.
                                                                                                                                                                                                                                         18-FEB-1997;
                                                            20-0CT-2000
                                                                                                                                                                                                                                                               19-APR-1993;
                                                                                                                                                                                                                                                                          29-JAN-1991;
                                                                                                                                                                                                 US6087560-A.
                                                                                                                                                                                                                       11-JUL-2000
                                         AAB07513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                   Peptide
12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187
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                                         δŏ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qq
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The inventors claim a new recombinant gene which codes for a protein with encochitinase activity, or its precursor (see AAQ21007). The coding part of the gene contains at least the 5' part of DNA for tomate endochitinase and at least the 3' part of DNA for the tobacce enzyme (DNA can be genomic or CDNA, but at least one intron is pref. present). The recombinant gene includes the 35S promoter of cauliflower mosaic virus plus the terminator from the nopaline synthase gene of Agrobacterium tumefaciens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pest-resistant plant; transformed plant; fungi; insect; bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toppan A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant protein with endo chitinase activity - encoding it and plants which express it, resistant to finsects, bacteria and nematodes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pignard A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence of endochitinase procursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                       AAR20822 standard; Protein; 328 AA.
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/label= cleavage
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                                                                                                                              213; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                          307 spgdnldcgngrsf 320
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                                                                                                                 Similarity
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Matches 213;
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                                                                                                                                                                       66 TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFATTG 124
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             125 SIDVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPG
                                                                                                      KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                          HDVITGRWSPSGADQAAGRVPGYGVITALINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plant
                                                                                                                                                                                                                                                                                                                                                                                                              oxalic acid degradation; oxalate oxidase; selection marker; tomato endochitinase; tobacco endochitinase; precursor; pathogen resistance; plant cell selection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of gene encoding oxalic acid degrading enzyme - for placell selection, esp. gene coupled to gene-encoding protein conferring pathogen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schneider M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grezes-Besset B, Grison R, Pignard A,
                                                                                                                                                                                                                                                                                                                                                                                     Endochitinase precursor coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25..75
/label= pro-sequence
76..329
/label= endochitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 34-37; 64pp; French.
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/label= pre-sequence
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                                                                                                                                                                                                                                                                                                      AAR56860 standard; Protein; 329 AA.
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(ERAP ) SOC NAT ELF AQUITAINE
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Nicotiana tabacum.
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                                                                                                                                                                                                                                                                                                                                AAR56860;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
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304
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                                                                                                                                                                                                                                                                                                                                                                                                          184
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                                                                                                                                                                                                                                    11; Gaps
                                                                                                                                                                                                                                                                                     65
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have been successfully transformed by the sequences are selected by their ability to grow on oxalic acid-contg. medium. AAR56860 is a known sequence of a precursor of endochitinase; the sequence was previously disclosed in W09201192.
                                                                                                                                                                                                                                                                                                              125 STDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                     7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                                       DB 15; Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi; dutch elm disease; E. coli; chitinase-like protein;
                                                                                                                                                                                       68.1%; Score 1202.5; DB 15; Lengt. 67.8%; Pred. No. 2.6e-91;
ive 38; Mismatches 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Mature chitinase-like protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "signal peptide"
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This sequence is encoded by the cDNA clone pHS2, and represents a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHS2 may be used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of elm trees.
                  Isolated chitinase gene derived from an American elm - used obtain prods. for inhibiting fungal infection of plants
                                                                                   Claim 1; Fig 1; 12pp; English.
                                                                                                                                                                                                                                                                                                            Sequence 317 AA;
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67.6%; Score 1192.5; DB 17; Length 317; 70.6%; Pred. No. 1.7e-90; Live 30; Mismatches 47; Indels 11; Query Match 67.6% Best Local Similarity 70.6% Matches 211; Conservative

., Έ SIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVAAFLAQ 139 11; Gaps 20 AEQCGSQAGGATCPNCLCCSKFGFCGTTSDXCGTGCQSQCNGCSGGTPVPVPTPSGGGVS 79 80 δă a ă g δ

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NYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGADQ 259 190

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Search completed: May 3, 2002, 18:30:32 Job time: 7551 sec

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                                                                               3, 2002, 18:43:04 ; Search time 79.44 Seconds (without alignments) 90.364 Million cell updates/sec
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1765
1 MRGVVVVAMLAAAFAVSAHA......DLLGVSYGDNLDCYNQRPFA
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6G_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FCTG_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/pcTG_COMB.pep:*
             Compugen Ltd.
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US-08-033-372-2

US-08-033-372-2

US-08-033-372-3

US-08-047-413-11

US-08-047-413-11

US-08-047-613-11

US-08-050-11

US-08-07-504-288C-6

US-08-379-259-6

US-08-379-259-6

US-08-379-259-8

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US-08-379-259-9

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US-08-448-398-3
GenCore version 4.5
Copyright (c) 1993 - 2000 Comy
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PRETIX, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
ZIP: 90071-2921
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPPERTUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
 US-08-047-413-9
US-08-229-050-9
US-07-791-931-8
US-07-791-931-9
US-07-791-931-9
US-08-162-475A-5
US-08-162-475A-4
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US-08-162-475A-4
US-08-329-799-37
US-08-329-799-35
US-08-329-799-36
US-08-329-799-36
US-08-329-799-36
US-08-329-799-36
US-08-329-259-14
US-08-329-259-14
US-08-349-389-9
US-08-349-389-9
US-08-349-389-9
US-08-349-389-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 22-WAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Reliter, Stephen E.
REGISTRATION NUMBER: 31,192
REPERBNEM/DOCKET NUMBER: P31 88
TELECOMMUNICATION 1970
TELECOMENICATION 1970
TELEFRONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/07704288C; Patent No. 5399680; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 336 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 73.7%
Best Local Similarity 72.3
Matches 237; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-704-288C-3
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SELRERERDASGG-----GGSGVASIVSESLFDLML.HERNDAACPASNFYIYDAFVA 112
                                                                                                  N-----GCSGGTPVPVPTFSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                                                                                                                                                             232 WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                                            AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                            YCTPSSQWPCAPGKKYFGRGFIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT
TITLE OF INVENTION: BLEENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.7%; Score 1301.5; DB 1
72.3%; Pred. No. 5.8e-111;
tive 27; Mismatches 47;
                                                                                                                                                                                                                                                                                                                    292 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                             293 IGFYRRYCDILGVSYGANLDCYSQRPSA 320
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/ABENT INFORMATION:
NAME: Reiter, Stephen E-
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/379, 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELERAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08379259
Patent No. 5695939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 amino acids
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CITY: Los Angeles
STATE: California
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Best Local Similarity
Matches 237; Conserva'
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US-08-379-259-3
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US-08-379-259-3
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                                                                                                        YCQQSAQWPCAAGKKYYGRGPIQLSYNFNYGPAGQAIGADLLGDPDLVASDATVSFDTAF 232
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                         :
SELRERERDDASGG------GGSGVASIVSRSLFDLMLLHRNDAACPASNFYTYDAFVA
                                                                               AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                            YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Maher, Eileen A.
APPLICANT: Dixob, Richard A.
TITLE OF INVENTION: TRANSCENIC PLANTS CONTAINING MULTIPLE TITLE OF INVENTION: DISEASE RESISTANCE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
AITONEY/AGENT INPORMATION:
NAME: Relier, Stephen E.
REGISTRATION NUMBER: 31,192
REGISTRATION NUMBER: 941 9391
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSEE: Pretty, Schroeder, Brueggemann & Clark 1: 444 South Flower Street, Suite 2000 Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
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72.3%; Pred. No. 5.8e-111;
iive 27; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                             293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
                                                                                                                                                                                                                                                                                                                      292 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Lamb, Christopher J.
APPLICANT: Zhu, Qun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 72.35
Matches 237; Conservative
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MEDIUM TYPE: Floppy
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ZIP: 90071-2921
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US-08-093-372-2
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APPLICANT: Cornelissen, Bernardus J.C.
APPLICANT: Meulenhoff, Elisabeth J.S.
APPLICANT: Meulenhoff, Elisabeth J.S.
APPLICANT: Van Roekel, Jeroen S.C.
APPLICANT: Sela-Buurlage, Marianne B.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: PUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 DVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURBENT APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70.9%; Score 1252; DB 1;
71.8%; Pred. No. 1.8e-106;
tive 29; Mismatches 51;
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APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-78A-1991
ATTOMELY AGENT INFORMATION:
NAME: MULESHING, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20025
TELECOMUNICATION INFORMATION:
TELECHOME: 415-494-0792
                                                                                                                                                                                                                                                                                                                                                          3: Morrison & Foerster
755 Page Mill Road
                          Sequence 11, Application US/08047413
Patent No. 5670706
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   324 amino acids amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Morrison
STREET: 755 Page Mi
CITY: Palo Alto
STATE: California
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              US-08-047-413-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 AFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                                                                         61 SPLRRRRPDASGG------GSSGYASIVSRSLFDLMLHRNDAACPASNFYTYDAFVA 112
                                                                                                                                                                                                                                                                                                     232 WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR 291
                                                                        N-----GCSGGTPVPPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
                                                                                                                                                113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD 171
                                                                                                                                                                                                                             YCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTAL 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 VSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTPVPVPTPS 74
1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC 59
                                  1 MRALAVVAMVARPFLAAAVHAEQCGSQAGGAVCPNCLCCSQFGWCGSTSDYCGAGCQSQC 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.2%; Score 1257; DB 4; 73.7%; Pred. No. 5.9e-107; rative 26; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Nettle Lectin cDNA FILE REFERENCE: MSG 4.1-114 CURRENT APPLICATION NUMBER: US/07/791,931C CURRENT FILING DATE: 1991-11-12 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 6 LENGTH: 310
                                                                                                                                                                                                                                                                                                                                                                                    292 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                        293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-07-791-931-6; Sequence 6, Application US/07791931C; Patent No. 6133507; BENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Nicotiana tabacum
US-07-791-931-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 224; Conservative
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Best Local Similarity
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APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
IITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                            247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                       127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
FILING DATE: US/08/801,563
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Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
Sela-Burlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTOMENY/AGENT INFORMATION:
NAME: MALASHIGG, KALE H.
REGISTRATION NUMBER: 29,959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11, Application US/08801563 Patent No. 6087560
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755 Page Mill Road
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TELEPHONE: 415-813-5600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 324 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                           307 GDNLDCYNQRPF 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 410 TELEFAX: 706141
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Sequence 11, Application US/08229050
Sequence 11, Application US/08229050
Setent No. 6066491
Setent No. 6066491
Setent No. 6066491
Setent Normalissen, Bernardus J.C.
APPLICANT: Melchers, Leo S. Applicant: Melchers, Leo S. Applicant: Welchers, Jacoen S.C.
APPLICANT: Vloemans, Alexandra A. APPLICANT: Vloemans, Alexandra A. APPLICANT: Woloshuk, Charles P. APPLICANT: Unithorst, Hubertus J.M. APPLICANT: Linthorst, Hubertus J.M. TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: OPLYNUCLEOTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.
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                           247 VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                  Gaps
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29; Mismatches 51.
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APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/229,050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Murashige, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX: 415-494-0792
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 71.89
Matches 224; Conservative
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ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                   304 GDNLDCGNQRSF 315
                                                                                                          GDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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US-08-229-050-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                           RESULT 6
US-08-229-050-11
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75 GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVA 134
                                                                                                                                                                                                                                                                     135 AFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                                                                                                                                                                                                                                               ISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSP 254
                                                                                                                                                                                                                                                                                                                                                                  255 SGADQAAGRVPCYGVIINIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
                                                                                                                    16 VSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTPVPVPTPS 74
                                                                                                                                          70.6%; Score 1246.5; DB 1; Length 310; 73.7%; Pred. No. 5.4e-106; Live 26; Mismatches 45; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE GENES AND PLANT
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE 25
CORRESPONDENCE 25
ADDRESSE: PRETTY, SCHENEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8899
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Patent No. 5695939
GENERAL INFORMATION:
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Stephen E.
31,192
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TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 444 South Flower CITY: Los Angeles STATE: California COUNTRY: United States ZIP: 90071-2921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     310 amino acids
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SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
                                                                      Best Local Similarity 73.79
Matches 224; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter, Stephe REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     315 QRPF 318
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US-07-704-288C-6
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US-08-379-259-6
                                                      Query Match
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                            127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                  187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                                                                            247 VITGEWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                      Gaps
                                                                                                                            8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT 66
                                                                                         ώ.
                                                      Length 324;
                                                                                           Indels
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et, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
                                                      Score 1252; DB 3;
Pred. No. 1.8e-106;
                                                                                           29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
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TELEFAX: (619) 546-9392
                                                      70.9%;
71.8%;
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COUNTRY: United States
ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 310 amino acids
amino acid
                                                                                             Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 GDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              304 GDNLDCGNQRSF 315
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                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-704-288C-6
                                                                                           224;
     US-08-801-563-11
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Recombinant gene coding for a protein having endochitinase activity or for a precursor thereof.
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184 PGRKYFGRGPIQISHNYNYGPCGRAIGVDLLNNPDLVATDPVISFKTALWFWMTPQSPKP 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGG
                                  Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.1%; Score 1202.5; DB 2 67.8%; Pred. No. 5.9e-102; ive 38; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEE: Foley & Lardner: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                           APPLICANT: DUBOIS, Michel APPLICANT: GRISON, Rene APPLICANT: LEGUAY, Jean-Jacques APPLICANT: PIGNARD, Annie APPLICANT: TOPPAN, Alain TITLE OF INVENTION: Recombinant grittle OF INVENTION: having endoch
                                                                                                                                                                                                                                    Sequence 13, Application US/08475427 Patent No. 5859340 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 67.8
Matches 213; Conservative
                                                                                                             GVSYGDNLDCYNQRPF 318
                                                                                                                                                 304 GVTPGDNLDCVNQRWF 319
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US-08-475-427-13
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US-08-475-427-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGDINARKREIAAFFAQTSHETTGGWASAPDGPYAWGYCFLRERGNPGDYCPPSSQWPCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALMFWMTPQSPKP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGGGPGPGP---GGDLGSAISNSMFDQMLKHRNENSCQGKNFYSYNAFINAARSFPGFGT 123
                                                                                                                                                                                                                                                                                                                                                                          75 GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVA 134
                                                                                                                                                                                                                                                                                                   135 AFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                              195 ISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGADOAAGRVPGYGVITNIINGGLECGRGODGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                         16 VSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTPVPVPTPS 74
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                                                                                                                                  DB 1; Length 310;
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                                                                                                                                                                      Indels
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Pred. No. 1.9e-102;
1; Mismatches 57;
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                                                                                                                                  Score 1246.5; DB 1
Pred. No. 5.4e-106;
                                                                                                                                                                    26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Raikhel, Natasha V.
IITE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SCOFWARE: Patentin Ver. 2.0
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/07791931C Patent No. 6133507 GENERAL INFORMATION:
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ilarity 69.0%;
Conservative 31
                                                                                                                                    70.68;
73.78;
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                                                                                                                                    Query Match 70.6
Best Local Similarity 73.7
Matches 224; Conservative
         TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
                                        ; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-379-259-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 218; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          315 QRPF 318
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APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
                                                              127 DINARKREIAAFFAQTSHETTGGWPSAPDGPFAWGYCFLRERGNPGDYCSPSSQWPCAPG 186
                                                                                                                                                                                                  KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
                                       66 TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFAITG 124
                                                                                                                       SIDVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                  245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
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16 LVLLSAAL----AQNCGSQGGGKVCASGQCCSKFGWCGNTNDHCGSGNCQSQ----CPGG 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: PRETIY, SCHROEDER, BRUEGGEMANN & CLARK 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704.2RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
68.1%; Score 1202; DB 1;
Best Local Similarity 68.7%; Pred. No. 6.6e-102;
Matches 217; Conservative 31; Mismatches 58;
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22-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/07704288C Patent No. 5399680 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: P:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 330 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (619) 546-47.
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 90071-2921
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CITY: Los Angeles
STATE: California
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US-07-704-288C-8
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      185 KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKFSS 244
                                                                                                                                                                       Gaps
                                                                SIDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSE: FOLEY & LARDNER
STREET: King Street Station, Suite 500,1800 Diagonal
STREET: Road, PO Box 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 1202.5; DB 2
; Pred. No. 5.9e-102;
38; Mismatches 52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gr
TITLE OF INVENTION: haring endoch
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/07842165
Patent No. 5932698
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 167
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 899149
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
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67.8%;
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(703) 683-4109
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AMINO ACID
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Best Local Similarity 67.83
Matches 213; Conservative
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CLASSIFICATION: 435
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                       307 SPGDNLDCGNQRSF 320
                                                                                                                                                                                                                                                                                                             SYGDNLDCYNQRPF 318
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US-07-842-165-13
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328
Matches 217;
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                                                PGGGPGPGP---GGDLGSAISNSMFDQMLKHRNENSCQGKNFYSYNAFINAARSFPGFGT 123
                                                                                                                                                                                                SSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLL 302
                                                                                    TGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCA 182
                            63 SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                          PCKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKP
                                                                                                                                                         10 VAYLLFSLLVLVESAALAQNCGSQGGGKACASGQCCSKFGWCGNTNDYCGSGNCQSQ---C
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: LANGE CHRISTOPHER J.
APPLICANT: LANGE CONN.
APPLICANT: LANGE OUN
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: REFTY, SCHROEDER, BRUEGGEMANN & CLAI
STREET: 444 SOUth Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELEPOMDUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEPHONE: (619) 546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/704,288
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08379259 Patent No. 5695939
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&
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 330 amino acids
amino acid
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                                                                                                                                                                                                                                                          303 GVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: United State ZIP: 90071-2921 COMPUTER READABLE FORM:
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STATE: California
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GENERAL INFORMATION:
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MOLECULE TYF
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                                                                                                                                                                                                                  63 SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                   PGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKP 242
                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                                                                             123 IGSTDVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14 GVVWMLLLVG----GSYGEQCGRQAGGALCFGGNCCSQFGWCGSTTDYCGPGCQSQCGG-68
  Gaps
                                       7 VAMIAAAFAV---SAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGC 62
                                                                          10 VAYLLESLLVLVSAALAQNCGSQGGGKACASGQCCSKFGWCGNTNDYCGSGNCQSQ---C 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALMFWMTPQSPKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123 TGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCA
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10;
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  Indels
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67.1%; Pred. No. 3.5e-100;
Live 36; Mismatches 54;
  58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Raikhel, Natasha V.
TITLE OF INVENTION: Nettle Lectin CDNA
FILE REFERENCE: MSU 4.1-114
CURRENT APPLICATION NUMBER: US/07/791,931C
CURRENT FILING DATE: 1991-11-12
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 7
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-791-931-7
; Sequence 7, Application US/07791931C
; Patent No. 6133507
  31;
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US-07-791-931-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         300 GVGYGNNLDCYSQTPF 315
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  Conservative
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4,

Length 330

Score 1202; DB 1; Pred. No. 6.6e-102;

68.1**%**; 68.7**%**;

Query Match Best Local Similarity

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666.2
666.2
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8.8
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8.4
1168.5
1167.5
1162
    33
                                                                                                     3, 2002, 18:32:12 ; Search time 88.01 Seconds (without alignments) 276.101 Million cell updates/sec
                                                                                                                                                              US-09-534-229C-3
1765
1 MRGVVVVAMLAAAFAVSAHA......DLLGVSYGDNLDCXNQRPFA 319
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                  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                219241 segs, 76174552 residues
                                                                           OM protein - protein search, using sw model
                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                      seq length: 0
seq length: 200000000
                                                                                                           Мау
                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                       Scoring table:
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Maximum DB s
                                                                                                                                                                                            Sequence:
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	30 1168.5 66.2 327 1 700965 Chitinase (EC 3: 31 1167.5 66.1 329 2 706999 Chitinase (EC 3: 31 1167.5 66.1 320 2 706999 Chitinase (Lass 3: 1165.6 65.5 308 2 702253 Chitinase (Lass 3: 1164.5 66.4 310.2 7.10810 Chitinase (EC 3: 31 1167.5 65.4 310.2 7.10810 Chitinase (EC 3: 31 1167.5 65.4 310.2 7.10810 Chitinase (EC 3: 31 1120 63.5 241.2 370026 Chitinase (EC 3: 31 1120 63.5 37.3 263.2 264.2 84030 Chitinase (EC 3: 31 1004.5 57.3 263.2 84030 Chitinase (EC 3: 31 1004.5 57.3 340.2 84030 Chitinase (EC 3: 31 1004.5 57.3 340.2 84030 Chitinase (EC 3: 2.1.14) - wheat Chitinase (EC 3: 2.144) - wheat
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CCSGGGTPVPVTFTESGGGVSSIISQSLFDQMLLHRNDAACQAKGFYNYGAFVAAANSFSG 120 239 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299 RESULT 2 JC2071 chitinase (EC 3.2.1.14) a - rye 61 180 181 240 241 300 301 qq g qq ΟŽ QΥ 8 4 QΥ οg δ

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Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; Keywords: glycosidase; hydrolase; lectronain: hevein chitin-binding domain homology <HCB>;21-62/Domain: hevein chitin-binding domain homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and chromosomal location of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chitinase (EC 3.2.1.14) - rice
NiAlternate names: endochitinase
CiSpecies: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Species: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C;Accession: T03614
R;Mishizawa, Y; Kishimoto, N; Saito, A; Hibi, T.
M;Michie: Sequence variation, differential expression and chromosomal location of A;Accession: T03614
A;Reference number: S39979; MUID:94049667
A;Residues: 1-323 Aux;
A;Genetics:
C;Genetics:
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homo C;Superfamil: plant chitin-binding domain homology <PCB>
F;82-627Domain: plant chitinase homology <PCB>
F;82-527Domain: plant chitinase homology <PCB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G-CSGGTPVPVPTPSGG---GVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANS
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                                                                                                                                                                                                                                                                                                                                                                  120 FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW
                                                                                                                                                                                               PCAPGKKYFGRGPIQ1SHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                                   240 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC
                           GCSGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG
MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 77.0%; Score 1359.5; DB Local Similarity 75.6%; Pred. No. 7.3e-94; nes 245; Conservative 27; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 DILGVGYGNNLDCYSQRPFA 318
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A; Experimental source: cv. NK1558
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C; Reywords: glycosidase; hydrolase; polysaccharide degradation
F;1-19/Domain: signal sequence #status predicted < CMAT>
F;20-318/Product: chtinase #status predicted < CMAT>
F;20-60/Domain: hevein chitin-binding domain homology <HCB>
F;80-318/Domain: plant chitinase homology <PCH>
             C;Species: Secale cereale (rye)
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 07-May-1999
C;Accession: 402071
R;Yamagami, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 58, 322-329, 1994
A;Attle: The complete amino acid sequence of chitinase-a from the seeds of rye (Secale A; Reference number: JC2071; MuID:94169514
A;Accession: JC2071
A;Residues: 1302 c7AM>
C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; C;Reywords: 91yosidase; hydrolase; polysaccharide degradation
F;142/Domain: hevein chitin-binding domain homology <PCE>
F;64-302/Domain: plant chitinase homology <PCE>
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R; Ignatius, S.M.J; Huang, J.; Muthukrishnan, S.

Submitted to the EMBL Data Library, September 1993

A; Description: Isolation and characterization of a barley chitinase genomic A; Reference number: 215336

A; Reference number: 215336

A; Accession: T04403

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DA.

A; Molecule type: DA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable chitinase (EC 3.2.1.14) precursor - barley
C;Species: Hordeum vilgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYNQRP 317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AQTSHETIGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQISH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGSTDVKKREVAAFL 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 EQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGC-SGGTPV-PVPTPS-GGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGA
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77.8%; Pred. No. 2e-97;
                                                                                                                                                                                                                                                                                                                                                              80.3%; Score 1416.5; Dl
82.1%; Pred. No. 4e-98;
iive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Mismatches
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Best Local Similarity 82.1%
Matches 248; Conservative
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Best Local Similarity
Matches 249; Conserv
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FA 302
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C; Species: Organ sativa (rice)
C; Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C; Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C; Accession: S15997
Nol. Gen. Genet. 226, 289-296, 1991
A; Their isolation and characterization of a rice gene encoding a basic chitinase.
A; Reference number: S15997; MUID: 91238706
A; Reference number: S15997
A; Reference number: S15
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                                                                                                                                                                                                                                                                                                                          SIDVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 NIETRKREVAAFLGQISHETIGGWPIAPDGPFSWGYCFKQEQNPPSDYCQPSPEWPCAPG 194
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                                                                                                                                                                                                                     KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
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Best Local Similarity 72.3%; Pred. No. 1.5e-89;
Matches 237; Conservative 27; Mismatches 47; Indels 17;
                                                                                                                               2;
                                                                             Length 339;
                                                                             Score 1313; DB 2; Length 3 Pred. No. 2.2e-90; Mismatches 47; Indels
                                                                                                                                 36; Mismatches
F;91-329/Domain: plant chitinase homology <PCH>
                                                                                74.48;
72.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S15997
chitinase (EC 3.2.1.14) - rice
                                                                                   Query Match 74.49
Best Local Similarity 72.99
Matches 229; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 GTGGNLDCYNQRPF 328
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A; Residues: 1-339 <NIS>
A; Cross-references: EMBL:X56787
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl. C; Reywords: glycosidase; hydrolase; polysaccharide degradation
C; Reywords: glycosidase; hydrolase; polysaccharide degradation
F; 33-74/Domain: hevein chitin-binding domain homology <HCB>
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C;Date: 18-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 10-Jul-1998
C;Dates: 38979
C;Accession: 539979
R;Nishizawa, Y.; Kishimoto, N.; Saito, A.; Hibi, T.
Mol. Gen. Genet. 241, 1-10, 1993
A;Title: Sequence variation, differential expression and chromosomal location of rice A;Recession: 539979; MUID: 94049667
A;Status: preliminary
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL:X56787; NID:g407471; PIDN:CAA40107.1; PID:g407472
C; Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology;
C; Keywords: glycosidase; hydrolase; polysaccharide degradation
F; 33-74, Domain: hevein chitin-binding domain homology <HCB>
F; 33-74, Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                     C;Species: Oryza sativa (rice)
C;Date: 25-Dec-1994 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAFT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
74.6%; Score 1317.5; DB 2;
Best Local Similarity 72.4%; Pred. No. 1e-90;
Matches 228; Conservative 36; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, November 1990
                                                                  298 YKRYCDMLGVSYGANLDCYNQRPF 321
                                        295 YKRYCDLLGVSYGDNLDCYNQRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chitinase (EC 3.2.1.14) - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGTGGNLDCYNQRPF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 VSYGDNLDCYNORPF 318
                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: S40414
A;Accession: S40414
A;Status: preliminary
                                                                                                                                                                                                                                 chitinase (EC 3.2.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-340 <NIS>
                                                                                                                                                                                                                                                                                                               C; Accession: S40414
R; Nishizawa, Y.
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Gaps

3;

Length 318; Indels

DB 2; 26;

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Sudbary

Sudbary

Sudbary

Sudbary

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Sudbary

Sudbary

C; Species: Nicotiana tabacum (common tobacco)

C; Species: Nicotiana tabacum (common tobacco)

C; Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 22-Jun-1999

C; Accession: S08627; JQ0993; Species: Sudbary

R; Shinshi, H:, Neuhaus, J.M.; Ryals, J.; Meins Jr., F.

R; Shinshi, H:, Neuhaus, J.M.; Ryals, J.; Meins Jr., F.

R; Shinshi, H:, Setzerier

A; Reference number: S08627; MUID: 91346623

A; Respecianental source: C. Havana 425

R; Neale, A.D.; Wahleithner, J.A.; Lund, M.; Bonnett, H.T.; Kelly, A.; Meeks-Wagner, D

R; Neale, A.D.; Wahleithner, J. 3-glucanase, osmotin, and extensin are expressed in tobacc

A; Reference number: JQ0993; MUID: 92404740

A; Accession: JQ0993

A; Accession: JQ0993

A; Residues: 1-72, H', 74, TRC', 79-262, 'S', 264-329 < NEA>

A; Cross-references: GB: 544869; NID: 9256132; PIDN: AAB23374.1; PID: 9256133

A; Cross-references: CB: 544869; NID: 9256132; PIDN: AAB23374.1; PID: 9256133

A; Cross-references: CB: 544869; NID: 9256132; PIDN: AAB23374.1; PID: 9256133

A; Cross-references: Lhin cell layer, cv. samsun nn

C; Comment: This protein is expressed mainly in roots.

C; Genetics: 148/1, 1997.

A; Introns: 148/1, 1997.

A; Introns: 148/1, 1997.

A; Introns: 148/1, 1997.

A; Introns: 148/1, 1997.

A; Accession: 148/1, 1997.

A; Introns: 148/1
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61 GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                                                                                                                                                                                                                                                                                    1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                                                                                                                  121 ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQE-RGATSDYCTPSSQW
                                                                                                                                                                                                                                  Score 1289.5; DB pred, No. 1.1e-88;
                                                                                                                                                                                                                                                                                          24; Mismatches
                                                                                                                                                                                                                                     73.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              300 DLLGVSYGDNLDCYNQRPF 318
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                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          234;
                                                                                                                                                                                                                                                                   Best Loca
Matches
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Richab, R.; Skriver, K.; Knudsen, S.; Ruud-Hansen, J.; Raikhel, N.V.; Mundy, J.
Plant J. 6, 579-589, 1994
A.Filte: Identification of an enhancer/silencer sequence directing the aleurone-specific
A.Filte: Identification of an enhancer/silencer sequence directing the aleurone-specific
A.Filte: Identification of an enhancer/silencer sequence directing the aleurone-specific
A.Filte: Inserting the aleurone-specific
A.Filte: Inserting translated from GB/EMBL/DDBJ
A.Filte: Inserting translated from GB/EMBL/DDBJ
A.Filte: Inserting translated from GB/EMBL/DBJ
A.Filte: Inserting translated from GB/EMBL/DBJ
A.Filte: CHI33
C.Superfamily: lectin-related plant chitinase; hevein chitin-binding domain homology; pl
C. Keywords: Glycosidase; hydrolase; polysaccharide degradation
F. 28-69/Domain: hevein chitinase homology <PCH>
F. 28-69/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Oryza sativa (rice)
C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Date: 21-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 22-Jun-1999
C;Accession: S14948
A;Tether Nucleotide sequence of a rice genomic clone that encodes a class I endochitinas A;Accession: S14948; MUID:91370895
A;Accession: S14948
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                   probable chitinase (EC 3.2.1.14) - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCQSQCNGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRN---DAACLAKGFYNYGAF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTA 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MRG------VVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGT
  17;
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                                                                                 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
                                                                                                               chitinase (EC 3.2.1.14) - rice
N;Alternate names: class I endochitinase
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71.6%;
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N.Alternate names: CHN50 protein; endochitinase
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 16-Sep-1992 #equence-1992 #text_change 22-Jun-1999
C;Accession: S20981; A29074; S13322; S19855
R;Van Buuren, M.; Neuhaus, J.M.; Shinshi, H.; Ryals, J.; Meins Jr., F.
Mol. Gen. Genet. 232, 460-469, 1992
A;Itle: The structure and regulation of homeologous tobacco endochitinase g
A;Reference number: S20981; MUD:92269767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCSGGTPVPVPTPSGG--GVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFS 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 GEATIGSIDVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAI--SDYCIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.1%; Score 1272.5; DB 2; 73.0%; Pred. No. 2.1e-87; tive 29; Mismatches 49;
                                                                                                                                                                                                                                                                                 chitinase (EC 3.2.1.14) class I, CH16 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: nucleic acid sequence not shown A;Molecule type: DNA
                                                                   DRIGEYKRYCDLLGVSYGDNLDCYNQRPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RYCDLLGVSYGDNLDCYNQRPF 318
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Matches 235; Conservative
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Best Local Similarity
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children (C. 2.2.1.14) class I precursor - rice
children (C. 2.2.1.19) children (C. 2.2.101.1995 children (C. 2.2.101.1999 children (C. 2.2.101.1999 children (C. 2.2.101.1999 children (C. 2.2.101.1996 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 ALWFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVA 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 AFWFWMTPQSPKPSCHAVMTGQWTPNGNDQAAGRVPGYGVTNIINGGVECGHGADSRVA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           112 AAANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT-- 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----NGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFV 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                            PVPVPTPSGGG-VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC- 59
                                                                                                                                                 99
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                                                                                                                                                 8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                         SLLFSLLLLSASAEQCGSQAGGARCPSGLCCSKFGWCGNTNDYCGPGNCQSQCPG--GPT
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           Length 329;
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                                                                              Indels
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           DB
                                            4.6e-88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Mismatches
       Score 1281.5;
Pred. No. 4.6e
                                                                              29; Mismatches
T2.6%;
Local Similarity 73.2%;
nes 229; Conservative 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 YGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 PGDNLDCGNQRSF 320
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Best Local Similarity
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              Query Match
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                                                    Best Loca
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chitinase (EC 3.2.1.14) class I precursor (clone ChtB3) - potato (fragment)
N;Alternate names: basic chitinase precursor
C;Species: Solanum tuberosum (potato)
C;Species: 20-oct-1994 #sequence_revision 01-Sep-1995 #text_change 22-Jun-1999
C;Accession: 543317; S06161
R;Beerhues, L.; Kombrink, E.
Piant Mol. Biol. 24, 333-367, 1994
A;Title: Primary structure and expression of mRNAs encoding basic chitinase and 1,3-b
A;Reference number: 543317; MUID:94154255
A;Accession: 543317
A;Molecule type: mRNA
A;Residues: 1-318 <BEE>
A;Cross-references: EMBL:U02607; NID:9467823; PIDN:AAA17409.1; PID:9467824
R;Laflamme, D.; Roxby, R.
Plant Mol. Biol. 13, 249-250, 1989
A;Title: Isolation and nucleotide sequence of cDNA clones encoding potato chitinase g
A;Reference number: S06161; MUID:92003671
A;Accession: S06161
A;Reference number: EMBL:X14133; NID:921465; A;Cross-references: EMBL:X14133; NID:921464; PIDN:CAA32351.1; PID:921465
A;Cross-references: EMBL:X14133; NID:921464; PIDN:CAA32351.1; PID:921465
A;Note: the authors translated the codon CAG for residues 54 and 303 as Gly, YGC for
A;Cross-references: EMBL:U02605; NID:9467819; PIDN:AAA18332.1; PID:9467820 C;Superfamily: lectin-related plant chitinase; hevein chitin-binding domain C;Keywords: glycosidase; hydrolase F:19-61/Domain: hevein chitin-binding domain homology <HCB> F:19-61/Domain: plant chitin-binding domain homology <HCB>
                                                                                                                                                                                                                                                                                                                                                                                                                                    68 VPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAKG-FYNYGAFVAAANSFSGFATTG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 STDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 MLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185 KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                                                                                              C;Superfamily: lectin-related plant chitinase; hevein chitin-binding C;Keywords: glycosidase; hydrolase; polysaccharide degradation C;Keywords: glycosidase; hydrolase; polysaccharide degradation E;11-18/Domain: signal sequence (fragment) #status predicted <ARI> F;19-311/Product: chitinase #status predicted <ARI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
                                                                                                                                                                                          DB 2;
                                                                                                                                                                                       71.1%; Score 1255.5; DB 2;
larity 72.6%; Pred. No. 3.8e-86;
Conservative 26; Mismatches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.8%; Score 1250.5; DB: 71.6%; Pred. No. 8.9e-86; ive 29; Mismatches 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 71.69
Matches 227; Conservative
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es 228; Conserv
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Matches
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                                                                                                                                               chitinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chitin-binding domain homology;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMLABARAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILFSILILSASAEQCGSQAGGARCASGLCCSKFGWCGNTNDYCGPGNCQSQCPG--GPT 68
                                                                                                                                               inhibition of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: EMBL:X51599; NID:g19844; PIDN:CAA35945.1; PID:g19845
                                          PID:919847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: lectin-related plant chitinase; hevein chitin-bi
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-324/Product: chitinase B #status predicted <ARI>F;24-66/Domain: hevein chitin-binding domain homology <HCB>F;78-316/Domain: plant chitinase homology <PCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                    A;Cross-references: EMBL:X64519; NID:g19846; PIDN:CAA45822.1;
                                                                                                                                                     enzyme:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%; Score 1261; DB 2; 72.1%; Pred. No. 1.5e-86; tive 29; Mismatches 50;
                                                                A.Experimental source: cv. Havana 425.
Kshinshi, H.; Mohmen, D.; Melns JT., F.
Proc. Mall. Acad. Sci. U.S.A. 84, 89-93, 1987.
A.Title: Regulation of a plant pathogenesis-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Solanum tuberosum (potato)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of mRNAs
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A;Molecule type: mRNA
A;Residues: 1-318 <BEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ribeerhues, L.; Kombrink, B.
Plant Mol. Biol. 24, 353-367, 1994
A/Fitle: Primary structure and expression
A/Reference number: S43317; MUID:94154255
A/Accession: S65019
                                                                                                                                                                                                                                                                                                                                    Plant Mol. Biol. 16, 1-10, 1991
A; Title: Gene structure and expression of
A; Reference number: S13322; MUID:91363829
                                                                                                                                                                                                                                                     A;Molecule type: mRNÅ
A;Residues: 15-324 <SHI>
R;Fukuda, Y;Ohme, M.; Shinshi,
Plant Mol. Biol. 16, 1-10, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cv. BY4
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                            A; Reference number: A29074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-324 <FUK>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Introns: 143/1; 194/2
                                                                                                                                                                                                                            A, Status: preliminary
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                                                                                                                                                                                                        A; Accession: A29074
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domain homology;

5;

Gaps

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Indels

Length 318;

<PRO>

Search completed: May 3, 2002, 18:32:13 Job time: 7476 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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- protein search, using sw model OM protein 3, 2002, 18:48:32; Search time 78.59 Seconds (without alignments) 148.824 Million cell updates/sec Мау Run on:

1 MRGVVVVAMLAAAFAVSAHA........DLLGVSYGDNLDCYNQRPFA 319 US-09-534-229C-3 1765 Perfect score: Title:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Sequence:

100059 seqs, 36664827 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P11955 hordeum	65 oryza sat	26 oryza	:52 ni	191 nicotian	.03 solanum	0.5	38	04	P36907 pisum sativ	526	115	92	90)23 b	.71 arabidopsi	513	215 phaseolus	66,	361 phaseolus	785 gossypi	969	951 hordeum	579 populus	337 lycopers	31 populus	021	061 populus	540 lycopersic	514 nicotiana	513 nicotiana	11218 urtica di	114 lycopersic
SUMMARIES	ΩΙ	CHI1_HOR	CHI2_ORYSA	- 1	~ I	- 1	- 1	CHI3_SOLTU		CHI2_SOLTU		CHI2_PEA	CHIT_SOLTU	CHI3_TOBAC	CHI4_SOLTU	CHI2_BRANA	CHIT_ARATH	CHIB_VITVI	CHIT_PHAVU	CHI1_GOSHI	CHI5_PHAVU	CHI2_GOSHI	CHI1_THECC	CHI2_HORVU	- 1	CHID_LYCES	CHIB_POPTR	- 1		CHIB_LYCES		P_TOB	_URT	CHIA_LYCCI
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d	Query Match	79	73.7	73.1	72.6	71.4	71.1	70.8	70.7	70.3	68.8	68.4	68.4	68.3	67.6	67.6	67.5	67.3	67.0	8.99	66.2	65.4	65.2	63.7	57.9	56.9	49.5	45.6	45.5	44.8	44.5	43.3	40.9	40.4
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	r S	1	2	m	4	D.	9	7	ထ	O)	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33

Q05539 lycopersico P42820 beta vulgar	P29023 zea mays (m Q06209 brassica na	P29022 zea mays (m P27054 phaseolus v	P80052 dioscorea j	P29032 populus tri P15326 coix lachry	Q06015 arachis hyp	-	Q06012 aracnıs nyp
CHIA_LYCES CHIP_BETVU	CHIB_MAIZE CHI4_BRANA	CHIA_MAIZE	CHIT_DIOJA	CHIC_POPTR IAMY COILA	CHI3_ARAHY	AGI_HORVU	CHIA_ARAHY
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253	269 268	280	250	121	46	212	46
39.2	34.0	32.7	28.5	16.8	11.8	11.6	11.4
692.5	599.5 579	577	503	297	208	205	201
34 35	36	38	0.4	41	1 es	44	45

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                           First. 12, Created)
01-007-1989 (Rel. 12, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOT-1997 (Rel. 35, Last annotation update)
101-NOT-1997 (Rel. 35, Last annotation update)
Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. HIMALAYA;
Swegle M., Huang J.-K., Lee G., Muthukrishnan S.;
"Identification of an endochitinase cDNA clone from barley aleurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- CATALYTIC ACTIVITY: HYDROIXSIS OF THE 1,4-BETA-LINKAGES OF N-ACCTYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- INDUCTION: BY ETHYLENE.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 12:403-412(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN-CV. NK 1558; TISSUE-Leaf; Ignatius S.M.J., Huang J., Muthukrishnan S.; Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                             318 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP, P23951, 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; I.
Pfam; PF00182; Glyco_hydro_19; I.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; I.
ProDom; PD000609; Chitin_bind; I.
SMART; SM00270; Chitbli, I.
PROSITE; PS00773; CHITINASE_19_1; I.
                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- FUNCTION: THIS PROTEIN FUNCT.
CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 141-318 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U02287; AAA18586.1; -. EMBL; X15349; CAA33407.1; -.
                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; S04131; S04131.
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NCBI_TaxID=4513;
                                                          CHI1_HORVU P11955;
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                           CHI1_HORVU
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DOMAIN
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                                                                                                                                                                                                                                                                                                120 FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQW 179
                                                                                                                                              1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- CATALYTIC STOTUTITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Bukaryota, Vitidiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
 CHITINASE_19_2; 1.
(dase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                 61 GCSGGTPVPVPTPS-GGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG
                                                                                                                                                                                                                                                     PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                Gen. Genet. 226:289-296(1991).
FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=91238706; PubMed=2034221; Zhu Q., Lamb C.J.; "Isolation and characterization of a rice gene encoding a basic chitinase.";
                                                                                                                               ω
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                                                                                                              DB 1; Length 318;
                        POTENTIAL.
26 KDA ENDOCHITINASE 1.
26 KDA ENDOCHITINASE 1.
27 SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
W, 42D62B2FE8041954 CRC64;
                                                                                                                               Indels
                                                                                                                               35;
                                                                                                             79.7%; Score 1407.5; DB 77.8%; Pred. No. 8.1e-99;
                                                                                                                                                                                                                                                                                                                                                                                                 336 AA
                                                                                                                                33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                           DLLGVSYGDNLDCYNQRPFA 319
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                        19
318
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33402 1
                                                                                                                                 Conservative
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 PS00774; CHITIN
e; Glycosidase;
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HSSP; P23951; 2BAA.
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318 AA;
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                                                                                                               Query Match
Best Local Similarity
Matches 249; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYDROLASES).
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          Hydrolase; Glyco:
Multigene family
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P25765;
                                           DOMAIN
DISULFID
DISULFID
                                                                     DISULFID
                                                                                       SEQUENCE
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CHI2_ORYSA
                            SIGNAL
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                                    CHAIN
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InterPro; IPR001002; Chitin_bind.

R InterPro; IPR001002; Chitin_bind.

R Ffam; PP00187; chitin_binding; 1.

R Ffam; PP00182; chyco_hydro_19; 1.

R FRINTS; PR00451; CHITINBINDNO.

R PRODOM; PR000574; GHYCO_hydro_19; 1.

R PRODOM; PR000570; Chitin_bind; 1.

R PROSITE; PS00070; CHITIN_BINDING; 1.

R PROSITE; PS00774; CHITINASE_19_1; 1.

R PROSITE; PS00774; CHITINASE_19_2; 1.

R Hydrolase; Ghycosidase; Chitin degradation; Chitin-binding; Signal; 3.

W Hydrolase family.

T SIGNAL

POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 N-----GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVA 112
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STRAIN-CV. JAPONICA; TISSUE-Seedling;
MEDLINE=91370895; PubMed=1893114;
Huang J.K., Wen L., Swegle M., Tran H.C., Thin T.H., Naylor H.M.,
Muthukrishnan S., Reeck G.R.;
"Nucleotide sequence of a rice genomic clone that encodes a class I endochitinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oryža sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
cnarmatonhvta; Magnoliophyta; Lillopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 AANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQER-GATSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 AASAFPGFAAAGDADINKREVAAFLAQISHEIIGGWAIAPDGPYIWGYCFKEENGGAGPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRGVVVVAMLAAAF-AVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 336;
                                                                                                                                                                                                                                                                         BASIC ENDOCHITINASE 2.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Indels
                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY.
7F4EC126265DEA84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                            73.7%; Score 1301.5; DB 72.3%; Pred. No. 7.6e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-WAR-1992 (Rel. 21, Created)
01-MAR-1992 (Rel. 21, Last sequence update)
01-DEC-1992 (Rel. 24, Last annotation update)
BASIC ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                318 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      293 IGFYKRYCDILGVSYGANLDCYSQRPSA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 IGFYKRYCDLLGVSYGDNLDCYNQRPFA 319
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BY
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M
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336
64
39
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35565 %
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                           336 AA;
                                                                                                                                                                                                                                                                                 222
222
333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237;
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DISULFID
DISULFID
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CHI1_TOBAC
P08252;
          CHIL_TOBAC
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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQE-RGATSDYCTPSSQW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 ATTRDADTCKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFKEENNGNAPTYCEPKPEW 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRALALAVVAMAVVAV--RGEQCGSQAGGALCPNCLCCSQYGWCGSTSDYCGAGCQSQCS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                     N-ACETYL-D-GLUCOSAMINB POLYMERS OF CHITIN.
-!- SIMILARITY: BELONGS TO CHITINARE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
Plant Mol. Biol. 16:479-480(1991).
-:- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :.
in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.1%; Score 1289.5; DB 1; Length 318; 73.4%; Pred. No. 5.7e-90; tive 24; Mismatches 56; Indels 5;
                           CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC ENDOCHITINASE 1.
CHITIN-BINDING (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                             PD000574; Glyco_hydro_19; 1. PD000609; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00026; CHITIN_BINDING; 1. PROSITE; PS00773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                        Interpro: IPR001002; Chitin_bind.
InterPro: IPR00726; Glyco_hydro_19.
Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
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                                                                                                                                                                                                                                                                                                                                                                                                           SM00270; ChtBD1;
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318
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318 AA;
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Multigene family.
SIGNAL
                                                                                                                    HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 234;
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                              SMART;
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                                                                                                                                                                                                                                                                                                                           Shinshi H., Neuhaus J.-M., Ryals J., Meins F. Jr., Structure of a tobacco endochitinase gene: evidence that different chitinase genes can arise by transposition of sequences encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -:- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.
-:- INDUCTION: BY ETHYLENE.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  containing proteins.";
Science 257:655-657(1992).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
CONTAINING FUNGAL PATHOGENS.
-!- CATALYTIC ACTIVITY: HYDROFINSIS OF THE 1,4-BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION.
MEDLINE-92052270; PubMed-1946457;
Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.;
Neuhaus J.M., Sticher L., Meins P. Jr., Boller T.;
A short C-terminal sequence is necessary and sufficient for the targeting of chitinases to the plant vacuole.";
Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr
"Vacuolar chitinases of tobacco: a new class of hydroxyproline-
                                  01-AUG-1988 (Rel. 08, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
01-AUG-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE A PRECURSOR (EC 3.2.1.14) (CHN-A).
329 AA.
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PTR; S08627; 808627.
HSSP; P29351; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19.
Pfam; PF00182; CHITINBINDNG.
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                                                                                                                                                                                                                                                                                      STRAIN-CV. HAVANA 425; TISSUE-Leaf;
MEDLINE-91346623; PubMed-1966383;
                                                                                                                                            Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                           cysteine-rich domain.";
Plant Mol. Biol. 14:357-368(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92358209; PubMed=1496378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydroxylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X16938; CAA34812.1; -.
STANDARD;
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                        Asteridae; euas
NCBI_TaxID=4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYDROXYLATION.
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MOD_RES
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                genes
HERERERE WAS REPRESENTED BREAK COCCOCCOCCOCCOCCETT RAY BREEK BAR BREEK B
                                                                                                                                                                                                                                                                                                 4;
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                                                                                                                                                                                                                                                                                                                                                                                                               TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KYFGRGPIQISHNYNGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 DYITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. HAVADMA 425; TISSUE-Leaf;
MEDLINE-92269767; Pubmed-1588915;
van Buuren M., Neuhaus J.-M., Shinshi H., Ryals J., Meins F. Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of a tobacco endochitinase gene in tobacco cells.";
                                                                                                                                                                                                                                                                                                                                                      8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
                                                                                                                                                                                                                                                                                                 'n
                        REMOVED IN MATURE FORM.
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
HYDROXYLATION.
                                                                                                                                                                                                                                                                Length 329;
                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                    HYDROXYLATION (PARTIAL).
3EC99D96E6C0114C CRC64
                                                                                                                                                                                                                                                                DB 1;
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01-MAR-1992 (Rel. 21, Last sequence update)
01-MAR-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE B PRECURSOR (EC 3.2.1.14) (CHN-B).
                                                                                                                                                                                                                                                                 Score 1281.5; DB Pred. No. 2.4e-89;
             ENDOCHITINASE A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               324 AA.
                                                                                                                                                                                      HYDROXYLATION
                                                                                                                                                                                                                                                                                                 29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. BRIGHT YELLOW 4; TISSUE=Leaf;
MEDLINE=913829; PubMed=1888899;
Fukuda Y., Ohme M., Shinshi H.;
"Gene structure and expression of a tobac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicotiana tabacum (Common tobacco).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Mol. Biol. 16:1-10(1991).
                                                                                                                                                                                                                      35156 MW;
                                                                                                                                                                                                                                                                   72.6%;
73.2%;
                                                                                                                                                                                                                                                                                                   Conservative
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3223
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659
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                   229;
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P24091;
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DISULFID
MOD_RES
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PIR; S13322; S13322.

PR; S13322; S13322.

PR; S20981; S20981.

PR; S20981; S20081.

PR; S20981; S20081.

PROSTOR: PF001802; Chitin_bind.

Probom; PF00187; Chitin_binding; 1.

PRINTS; PR00451; CHITINBINDNO.

PRODOM; PD0006054; CHITINBINDNO.

PRODOM; PD0006056; CHITINBINDNO.

PROSTIE; PS00770; Chtbl; 1.

PROSTIE; PS00774; CHITINASE_19_1; 1.

PROSTIE; PS00774; CHITINASE_19_1; 1.

PROSTIE; PS00774; CHITINASE_19_2; 1.

PROSTIE; PS00774; CHITINASE_19_2; 1.

PROSTIE; PS00774; CHITINASE_19_2; 1.
                                                                                                                                                                                        Shinshi H., Mohnen D., Meins F. Jr.; "Regulation of a plant pathogenesis-related enzyme: inhibition of chitinase and chitinase mRNA accumulation in cultured tobacco tissues
structure and regulation of homeologous tobacco endochitinases of Nicotiana sylvestris and N. tomentosiformis origin."; Gen. Genet. 232:460-469(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jr.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             containing proteins.";
Science 257:655-657(1992).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHIIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROXYLATION.
MEDLINE=92358209; PubMed=1496378;
Sticher L., Hofsteenge J., Milani A., Neuhaus J.M., Meins F. Jr
"Vacuolar chitinases of tobacco: a new class of hydroxyproline-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONTAINTIC ACTUITY: HUDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.

-: SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS.

-: INDUCTION: BY ETHYLENE:

-: SIMILARITY: BELONGS TO CHITTNAGE OF NEEDS OF NEEDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REMOVED IN MATURE FORM (PROBABLE) CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=92052270; PubMed=1946457; Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.; Neuhaus J.M., Sticher L., Meins F. Jr., Boller T.; Asbort C-traminal sequence is necessary and sufficient for targeting of chitinases to the plant vacuole."; Proc. Natl. Acad. Sci. U.S.A. 88:10362-10366(1991).
                                                                                                        [3]
SEQUENCE OF 15-324 FROM N.A., AND SEQUENCE OF 24-53.
                                                                                                                                                                                                                                                                                       by auxin and cytckinin.";
Proc. Natl. Acad. Sci. U.S.A. 84:89-93(1987).
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HYDROXYLATION.
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Hydroxylation, Multigene family.
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                                                                                                                                                                                                                                                                                    and cytokinin.";
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324
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65
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                                                                                                                                                              STRAIN=CV. HAVANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                       127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                   Gaps
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"Primary structure and expression of mRNAs encoding basic chitinase and 1,3-beta-glucanase in potato.";
Plant Mol. Biol. 24:353-367(1994).
-i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Magnoliophyta, eudicotyledons; core eudicots; Asteridae, euasterids I; Solanales; Solanaceae, Solanum.
                                                                                                                                                                                                                                                                 11 SLLFSLLLLSASAEQCGSQAGGARCASGLCCSKFGWCGNTNDXCGPGNCQSQCPG--GPT
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                                                                                                             Length 324;
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                        34721 MW; FA65DC2113B33EB6 CRC64;
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01-ocr-1996 (Rel. 34, Last sequence update)
01-ocr-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 1 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                         71.4%; Score 1261; DB 1;
72.1%; Pred. No. 8e-88;
tive 29; Mismatches 50;
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HYDROXYLATION.
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STRAIN=CV. DATURA; TISSUE=Leaf;
MEDLINE=94154255; Pubmed=8111037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONTAINING FUNGAL PATHOGENS
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                           324 AA;
                                                                                                                                                 Best Local Similarity
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                                                                                                                                                                         Matches 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 SIDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQWPCAPG 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
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REMOVED IN MATURE FORM, VACUOLAR
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BY SIMILARITY.
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01-0cr-1996 (Rel. 34, Last sequence update)
01-0cr-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                 71.1%; Score 1255.5; DE 72.6%; Pred. No. 2e-87;
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26; Mismatches
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                                                                                        Interpro; IPR001002; Chitin_bind.
Interpro; IPR0010726; GJYco_hydro_19.
Pfam; PP00187; Chitin_binding, 1.
Pfam; PP00182; GJYco_hydro_19; 1.
ProDom; PD000574; GJYco_hydro_19; 1.
ProDom; PD000509; Chitin_bind; 1.
SMART; SM00270; Chitin_bind; 1.
                                                                                                                                                                     SMART; SMO0270; ChtBD1; 1.
PROSTITE; PS0026; CHITIN_BINDING; 1.
PROSTITE; PS00773; CHITINASE_19_1; 1.
PROSTITE; PS00774; CHITINASE_19_2; 1.
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33813 MW;
                                                                 EMBL; U02605; AAA18332.1;
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P52405;
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CHI3_SOLTU
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Hydroxylation; Multigene family.
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                                                                                                                                   302 LGVSYGDNLDCYNQRPF 318
                                                                                                                                                 STANDARD;
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Q05538;
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                                                                                                                                             -:- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPIAST (BY SIMILARITY).
-:- DEVELOPMENTAL STRAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                    OLD ROOT SEGMENTS, AND CARPELS.
INDUCTION: IN RESPONSE TO INFECTION, ELECTIOR, ETHYLENE, WOUNDING.
SIMILARITH: BELONGS TO CHITINASE CLASS IS WHICH IS SIMILAR TO
CLASS IB IN THE CATALITIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 GTPVPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----GPGPSGDLGGV---ISNSMFDQMLNHRNDNACQGKNNFYSYNAFISAAGSFPGFG 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 TTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 VVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSG 64
                                                                        Beerhues L., Kombrink E.; "Primary structure and expression of mRNAs encoding basic chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                and 1,3-beta-glucanase in potato.";
Plant Mol. Biol. 24:353-367(1994).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENDOCHITINASE 3.
REMOVED IN MATURE FORM, VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TARGETING (POTENTIAL).
CHITIN-BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         46; Indels
euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY.
BF587A8515534E71 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.8e-87
; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.8%; Score 1250.5; 71.6%; Pred. No. 4.8e
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001002; Chitin_bind.
InterPro; IPR000726; Glyco_hydro_19.
Pfam: PF00187; Chitin_binding; 1.
Pfam: PF00182; Glyco_hydro_19; 1.
Probom: PD000574; Glyco_hydro_19; 1.
Probom: PD000669; Chitin_bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE, PS00026; CHITIN BINDING; 1. PROSITE; PS00773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_2; 1.
                                                           MEDLINE=94154255; PubMed=8111037;
                                                                                                                                    CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                            |L|
SEQUENCE FROM N.A.
SEQUENCE FROM N.A. TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33798 MW;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U02607; AAA17409.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM00270; ChtBD1;
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Matches 227; Conserv
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19
312
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221
330
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                                                                                                                                                                                                                                                                                     HYDROLASES)
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DISULFID
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                                                                                                                                                                                                                                                                                                                   242 PSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDL 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00026; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase, Glycosidase; Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -:- CATALYTIC ACTIVITY: HYDROXYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-:- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-:- INDUCTION: BY FUNGAL INFECTION.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danhash N., Wagemakers C.A.M., van Kan J.A.L., de Wit P.J.G.M.;
"Molecular characterization of four chitinase cDNAs obtained from Cladosportum fulvum-infected tomato.";
Plant Mol. Biol. 22:1017-1029(1993).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                 182 APGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPK
                                                                                                                                                             Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicoryledons; core eudic
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
01-CT-1994 (Rel. 30, Last anoctation update)
BASIC 30 KDA ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
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STRAIN-CV. MONEYMAKER;
MEDLINE-94003061; PubMed-8400122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   322
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PISSP, P29251; ZBAA.

INTERPO, PRO01002; Chitin_bind.

InterPro; IPR001002; Chitin_bind.

Pfan; PF00187; chitin_binding; 1.

Pfan; PF00182; Glyco_hydro_19;

PRINTS; PR00451; CHITINBINDNG.

PF0DOm; PD000654; Glyco_hydro_19;

PF0DOm; P0000669; Chitin_bind; 1.

SMART; SM00270; ChtBD1; 1.
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-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-!- DEVELOPMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS SEGMENTS AND IN OLDER ONES. LEAVES AND STEMS OF INTERMEDIATE AGE SHOW A DECREASED EXPRESSION. APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --GPGPSGDLGGV---ISNSMEDQMINHRNDNACQGKNNFYSYNAFVTAAGSFPGFGTTG 119
                                                                                                                                                                                                                                                                                                                                                                   125 STDVKKREVAAFLAQISHETIGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPG 184
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                         68 VPVPTPSG--GGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFATTG 124
                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                9 MLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGTP 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Primary structure and expression of mRNAs encoding basic chitinase and 1.3-beta-qlucanase in potato."; Plant Mol. Biol. 24:353-357(1994).
-i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum (Potato).
Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
NCBL_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                            185 KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                            245 HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV
                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                     70.7%; Score 1248.5; DB 1; Length 322; 72.6%; Pred. No. 6.9e-87; Live 25; Mismatches 46; Indels 15;
                        REMOVED IN MATURE FORM.
CHITIN BINDING (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION (POTENTIAL).
            BASIC 30 KDA ENDOCHITINASE.
                                                                                                                               DROXYLATION (POTENTIAL). D13A9191AEE8FC5A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     316 AA.
                                                                                                                                HYDROXYLATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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STRAIN-CV. DATURA; TISSUE-Leaf;
MEDLINE-94154255; PubMed-8111037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONTAINING FUNGAL PATHOGENS.
                                                                                                                                             34345 MW;
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                                                                                                                                                                                       Query Match
Best Local Similarity 72.6*
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  305 SYGDNLDCYNQRPF 318
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3122
3123
3224
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652
662
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663
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3123
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322 AA;
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DISULFID
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MOD_RES
SEQUENCE
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PROPEP
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SIGNAL
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                                                                                                                                                                                                                                          HASSP, P23951; ZBRA.

R HASSP, P23951; ZBRA.

R HASSP, P23951; ZBRA.

R InterPro; IPR001002; Chitin_bind.

R Ffam; PF00182; Chyco_hydro_19.

R Profoun; P000187; Chitin_binding; 1.

R Profoun; P000187; Chitin_binding; 1.

R Profoun; P000180; Chitin_bind; 1.

R PROSITE; PS00774; CHITINASE 19_1; 1.

R PROSITE; PS00774; CHITINASE 19_2; 1.

R PROPEP 310 316 REMOVED IN MATCHE FORM, VACUOLAR

T PROPEP 310 316 REMOVED IN MATCHE FORM, VACUOLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 VIIGRWSPSGADQAAGRVPGYGVIINIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSY 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -:- INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
-:- SIMILARITY: BELONGS TO CHITINASE CLASS IN WHICH IS SIMILAR TO CLASS IB IN THE CAPALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 VPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKG-FYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 LLFSVLLLSASAEQCGSQAGGALCASGLCCSKFGWCGNTNDYCGPGNCQSQ---CPGGSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 316;
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BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81FB3DB3F222A0C6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.3%; Score 1240.5; DB 1; 70.8%; Pred. No. 2.7e-86; Live 31; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TARGETING (POTENTIAL
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42
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58
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33629 MW;
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                                                                     HYDROLASES)
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ID CHIX_PEA
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AFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKKYFGRGPIQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                             QRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                  316 QRSFA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHI2_PEA
P21226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
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                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Vicieae; Pisum. NCBL_TaxID=3888)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONTAINING FUNGAL PATHOGENS.
-!-CATALTYTC ACTIVITY: HYDROLYSIS OF THE 1,4 BETA-LINKAGES OF
N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
-!- INDUCTION: BY FUNGAL INFECTION.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LEGIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSGGTP-VPVPTPS
                                                                                                                                                                                                                                                                                                                                                                                                                                            chitinase mRNA from pea leaves (Pisum sativum L.) inoculated with Associate pisi Lib.";
Plant Sci. 92:69-79(1993).
-i- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4;
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                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. BIRTE; TISSUE=Leaf;
Vad K., de Neergaard E., Madriz-Ordenana K., Mikkelsen J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                     "Accumulation of defence-related transcripts and cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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7EDECRETAECC3435 CRC64;
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ENDOCHITINASE.
CHITIN-BINDING (BY S.
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                    01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-OCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
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InterPro; IPR001726; Glyco_hydro_19.
Pfam, PP00187; Chitin_binding; 1.
Pfam, PP00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000659; Glyco_hydro_19; 1.
Probom; PD000669; Chitin_bind; 1.
SMART; SM00270; ChtBD1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00026; CHITIN BINDING; 1. PROSITE; PS00773; CHITINASE_19_1; 1. PROSITE; PS00774; CHITINASE_19_2; 1.
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320
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58
320 AA;
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                                                                                                                                                                                                                                                                                                                                                                                          Collinge D.B.;
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SGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVSYGDNLDCYN 314
                                                                                                                                                                                                                                           SAADSSAGRVPGYGVITNIINGGIECGHGQDNRVDDRVGFYRRYCQIFGVDPGGNLDCNN 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. ALCAN;
MEDLINE=55306779; PubMed=7787175;
Chang M.M., Horovitz D., Culley D., Hadwiger L.A.;
Chang M.M., Horovitz D., Culley D., Hadwiger L.A.;
"Molecular cloning and characterization of a pea chitinase gene expressed in response to wounding, fungal infection and the elicitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chitinase isolated
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-!-SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO SIMILARITY: PALLYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pisum sativum (Garden pea).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons; core eudicots, Rosid
eurosids I; Fabales, Fabaceae, Papilionoideae, Vicieae, Pisum.
                                                                                       ISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHDVITGRWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
ENDOCHITINASE A2 PRECURSOR (EC 3.2.1.14).
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InterPro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
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Plant Mol. Biol. 28:105-111(1995).
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Gaynor J.J.;
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                                                                                                                                                                                                                                                                        TPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGS 125
                                                                                                                                                                                                                                                                                      ------GGTLSSLISGDTFNNMLKHRNDNACQGKPFYTYDAFLSAAKAFPNFANKGD 115
                                                                                                                                                                                                                                                                                                             TDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGK 185
                                                                                                                                                                                                                                                                                                                                 TATKKREIAAFLGQTSHETTGGWPTAPDGPYAWGYCFLREQN-PSTYCQASSEFPCASGK 174
                                                                                                                                                                                                                                                                                                                                                     KYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSH 245
                                                                                                                                                                                                                                                                                                                                                                   QYYGRGPIQISWNYNYGQCGRAIGYDLINNPDLVATDPYISFKTALWFWMTPQSPKPSCH 234
                                                                                                                                                                                                                                                                                                                                                                                             DVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGVS 305
                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis of a genomic clone encoding an endochitinase from Solanum tuberosum.";
                                                                                      ENDOCHITINASE A2.

REMOVED IN MATURE FORM (BY SIMILARITY).

CHITIN-BINDING (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

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                                                                                                                                                                                                              12; Gaps
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                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                          Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                           PROSITE; PS00026, CHITIN_BINDING; 1.
PROSITE; PS00773; CHITINASE 19 1; 1.
PROSITE; PS00774; CHITINASE 19 2; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Multigene family; Signal.
                                                                                                                                                                                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asteridae; euasterids I; Solanales; Solanaceae; Solanum
NCBI_TaxID-4113;
                                                                                                                                                  SIMILARITY.
540F0DA5EC1DC2FA CRC64;
                                                                                                                                                                                          DB 1;
                                                                                                                                                                                        68.4%; Score 1208; DB 1,
69.0%; Pred. No. 7.6e-84,
iive 31; Mismatches 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 17:5855-5855(1989)
         ; PD000574; Glyco_hydro_19; 1. SM00270; ChtBD1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-CV. RUSSET BURBANK;
MEDLINE-89345190; PubMed-2762165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-CV. RUSSET BURBANK;
MEDLINE-88262525; Pubmed-3387233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09, Created)
                                                                                                                                                59 E
 PRINTS; PR00451; CHITINBINDNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaynor J.J., Unkenholz K.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Solanum tuberosum (Potato).
                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                309
329
324
62
38
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                                                                                                                                                                                                                                                                                                                                                                                                                                               306 YGDNLDCYNQRPF 318
                                                                                                                                                             AA;
                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1988 (Rel.
                                                                                                                                                                                                            Matches 216;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHIT_SOLTU
                                                                                       CHAIN
PROPEP
DOMAIN
DISULFID
                                                                                                                                                                                          Query Match
Best Local (
                                                                                                                                         DISULFID
                                                                                                                                DISULFID
                                                                                                                                                   DISULFID
                                                                                                                                                           SEQUENCE
                                                                              SIGNAL
                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
CHIT_SOLTU
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"Přimary structure of an endochitinase mRNA from Solanum tuberosum.";
Nucleic Acids Res. 16:5210-5210(1988).
-!- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGKKYFGRGPIQISHNYNYGPASQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKP 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 SGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 TGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGDINARKREIAAFFAQISHETTGGWASAPDGPYAWGYCFLRERGNPGDYCPPSSQWPCA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 VAYLLFSLLVLVSAALAQNCGSQGGGKACASGQCCSKFGWCGNTNDYCGSGNCQSQ---C 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                              -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYLD-GLUCOSAMINE POLYMERS OF CHITIN.
-!- SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLAST (BY SIMILARITY).
-!- INDUCTION: BY ETHYLENE.
-!- SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHITIN-BINDING LECTIN DOMAIN (BELONGS TO PAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chitin degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REMOVED IN MATURE FORM (PROBABLE). CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.

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BY SIMILARITY.

669B82159BC176EF CRC64;
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31; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR, S05426, S05426.
HSSP, P23951, 2BAA.
InterPro; IPR001002, Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
PRIMTS; PR00451; Glyco_hydro_19; 1.
PRIMTS; PR00451; Glyco_hydro_19; 1.
PRODOM; PD000574; Glyco_hydro_19; 1.
SYDODOM; PD0000574; Glyco_hydro_19; 1.
SYDODOM; PD0000574; Glyco_hydro_19; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00270; ChtBbl; 1.
PROSITE; PS00026; CHTIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
                                                                                           CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΜW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62
328 AA;
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Query Match
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Matches
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CHI4_SOLTU
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PRINTS: PR00451; CHITINBINDNG.
ProDom; PD000654; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
PROSITE; PS00770; CHITIN_BINDING; 1.
PROSITE; PS00773; CHITIN_BINDING; 1.
PROSITE; PS00774; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_1; 1.
Hydrolase; Glycosidase; Chitin degradation; Chitin-binding; Signal; Hydrolase; Multigene family.
                                                                                                                                                                                                                                                        STRAIN—CV. HAVANA 425; TISSUE=Leaf;
MEDLINE=92209767; PubMed=158915;
MEDLINE=92209767; PubMed=158915;
"The Structure and regulation of homeologous tobacco endochitinase genes of Nicotiana sylvestris and N. tomentosiformis origin.";
Mol. Gen. Genet. 232:466-469(1992).
-I-FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN COMPAINING FUNGAL PATHOGENS.
-I-CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: VACUOLAR AND PROTOPLASTS (PROBABLE).
SIMILARTY: BELONGS TO CHTINRASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILK 19 OF GLYCOSYL
                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REMOVED IN MATURE FORM (PROBABLE). CHITIN-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
W; 4F684CEIFBD432FB CR644;
                                                                                                        01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
10-CCT-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE 3 PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENDOCHITINASE 3.
                                                                                   334 AA
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InterPro; IPR001002; Chitin_bind.
InterPro; IPR007025; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
                                                                                  PRT;
                                                                                                                                                                       Nicotiana tabacum (Common tobacco)
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           304 GVTPGDNLDCVNQRWF 319
GVSYGDNLDCYNQRPF 318
                                                                                   STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   HYDROLASES).
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67
69
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                                                                                 CHI3_TOBAC
P29059;
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MOD_RES
SEQUENCE
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SUBCELLULAR LOCATION: VACUOLAR AND PROTOFLAST (BY SIMILARITY).
DEVELOMENTAL STAGE: HIGHEST LEVELS IN YOUNGER LEAVES OR STEMS
SEGMENTS AND IN OLDER ONES, LEAVES AND STEMS OF INTERMEDITATE AGE
SHOW A DECREASED EXPRESSION, APPRECIABLE AMOUNTS ARE ALSO FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OLD ROOT SEGMENTS, AND CARPELS.
INDUCTION: IN RESPONSE TO INFECTION, ELICITOR, ETHYLENE, WOUNDING.
SIMILARITY: BELONGS TO CHITINASE CLASS IA WHICH IS SIMILAR TO
CLASS IB IN THE CATALYTIC PARE BUT WHICH INCLIDE A N-TERMINAL
CHITIN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
                                                                                                                                                                                                                                                123
                                                              Gaps
                                                                                                                                                                                 70
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MEDLINE=94154255; PubMed=3111037;
MEDLINE=94.54555; PubMed=3111037;
MEDRINES DATUS DATUS DATUS DESCRIPTION OF MRNAS encoding basic chitinase and 1,3-beta-glucanase in potato.";
Plant Mol. Biol. 24-353-367(1994).
-:- FUNCTION: THIS PROTEIN FUNCTIONS AS A DEFENSE AGAINST CHITIN CONTAINING FUNGAL PATHOGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                          SILVIFILLAVSARQCGKQAGGARCPSGMCCSNFGWCGNTQDYCGPGRCQSQCPSGPGFT
                                                                                                                                                                                                                                                                                       ---PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATT
                                                                                                                                                                                                                                                                                                                                                                             GSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          244 SHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLG
                                                                                                                         8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
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Length 334;
                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Last annotation update)
ENDOCHITINASE 4 PRECURSOR (EC 3.2.1.14) (FRAGMENT).
68.3%; Score 1206; DB 1; 67.9%; Pred. No. 1.1e-83; iive 32; Mismatches 65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequ
01-0CT-1996 (Rel. 34, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Solanum tuberosum (Potato)
                                                                 Conservative
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                                    Similarity
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SEQUENCE FROM N.A.
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                                       Local Sim
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completed: May
ne: 917 sec
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                                                                                                                                 HYDROLASES)
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SEQUENCE
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Matches 21
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agreement (See http://www.isb-sib.ch/announce/
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAK-GFYNYGAFVAAANSFSGFAFF 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 KPPTPGPGPSGGDIGSVISNSMFDQMLKHRNDNACQGKNNFYSYNAFINAARSFGGFGTT 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00270; ChtBD1; I.
PROSITE; PS00026; CHTIN_BINDING; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Hydrolase; Glycosidase; Chitin_degradation; Chitin-binding; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 VAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQC-NGCSG
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SEQUENCE FROM N.A.
MEDLINE=94143492; PubMed-8310072;
Hamel F., Bellemare G.;
"Nucleotide sequence of a Brassica napus endochitinase gene.";
Plant Physiol. 101:1403-1403(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B1E2F0D643B08284 CRC64;
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CHIILN-BINDING (BY S
BY SIMILARITY.
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01-ocr-1994 (Rel. 30, Last sequence update)
01-Cr-1994 (Rel. 30, Last annotation update)
ENDOCHITINASE CH25 PRECURSOR (EC 3.2.1.14).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
  entities requires a license agreement (or send an email to license@isb-sib.ch)
                                                                                                                                                           Interpro; IPR000726; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
ProDom; PD000574; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
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                                                                                                                                 InterPro, IPR001002; Chitin_bind.
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                                                                                 EMBL; U02608; AAA17410.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
es 210; Conserv
                                                                                                           HSSP; P23951; 2BAA.
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Multigene family.
NON_TER
SIGNAL <1
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CHI2_BRANA
CHI2_BRANA
CD1023
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DT 01-027
DF 01-027
DF ENDOCT
OC BUARY
OC BUARY
OC SPERME
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 NGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N-ACETYL-D-GLUCOSAMINE POLYMERS OF CHIIN.
-!- SIMILENITY: BELONGS TO CHIILNESS CLASS IA WHICH IS SIMILAR TO CLASS IB IN THE CATALYTIC PART BUT WHICH INCLUDE A N-TERMINAL CHIILN-BINDING LECTIN DOMAIN (BELONGS TO FAMILY 19 OF GLYCOSYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.6%; Score 1192.5; DB 1; Length 322;
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; Mismatches 58
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SIMILARITY.
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Interpro; IPR0010026; Glyco_hydro_19.
Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
ProDom; PD000574; Glyco_hydro_19; ProDom; PD000609; Chitin_bind; 1.
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HSSP; P23951; 2BAA.
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3, 2002, 18:47:01; Search time 157.87 Seconds (without alignments) 295.565 Million cell updates/sec
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1 MRGVVVVAMIAAAFAVSAHA......DLLGVSYGDNLDCXNQRPFA 319
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*
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sp_vertebrate:*
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Maximum DB seq length: 2000000000
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sp_plant:*
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
: ! ~~!	1696.5	96.1	 	10	041539	Q41539 triticum ae
7	1675.5	94.9		10	Q9AXR9	Q9axr9 secale cere
3	1597	90.5		10	69SQL3	Q9sql3 poa pratens
4	1557	88.2		10	Q9SQL4	
S	1421	80.5		10	Q9FRV1	
Ø	1359.5	77.0		10	042993	Q42993 oryza sativ
7	1352.5	76.6		10	042994	
ω	1317.5	74.6		10	043294	
σ	1305	73.9		10	P93680	P93680 persea amer
0	1291.5	73.2		10	042839	Q42839 hordeum vul
-	1279	72.5		10	042992	Q42992 oryza sativ
7	1274	72.2		10	042995	
e	1272.5	72.1		10	040667	
14	1260	71.4		10	041180	
'n	1256	71.2		10	09FS45	
9	1253	71.0		10	Q9FEW1	
17	1239.5	70.2	318	10	038777	Q38777 allium sati
18	1237	70.1		10	Q9SDY6	Q9sdy6 glycine max
σ	1236	70.0		10	042970	

	7	P94084 medicago sa				æ		0				Q43179 solanum tub	arabido			arabidop	Q9m7g7 arabis glab	arabidop	Q9m7g2 arabis lign	-	cacar	Q9ztk4 vitis vinif	vigna	аI	081144 solanum tub
Q9M7F5	P93327	P94084	Q9FXL8	Q9M7H2	038776	042428	081145	Q9M7H0	098735	098838	Q9M7H4	043179	Q9SXJ4	Q9M7G4	Q9M7G9	Q9SXJ2	Q9M7G7	Q9SXJ3	Q9M7G2	Q9M7F4	080404	Q92TK4	Q9FUH3	Q9ZP10	081144
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
312	325	327	315	305	302	316	329	326	335	335	308	315	335	302	310	335	320	335	306	312	311	325	297	328	329
68.5	68.5	68.4	68.3	68.3	68.2	68.0	67.9	67.7	67.5	67.5	67.4	67.2	67.2	67.2	67.2	67.2									
1208.5	1208.5	1207.5	1206	1205.5	1203.5	- :	1198.5	1194.5	1190.5	- 1	1189.5	1186.5	1186.5	1185.5		1185.5	1185	œ	1183.5	1181.5	1180	1177	1174.5	1171.5	1167.5
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 1

041539

AC 041539;

AC 041539;

CAL 041539;

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1996 (TrEMBLrel. 17, Last annotation update)

DT 01-NOV-1996 (TrEMBLrel. 17, Last annotation update)

DT 01-NOV-1996 (TrEMBLrel. 17, Last annotation update)

DT 01-JUN-2010 (TrEMBLrel. 17, Last annotation update)

DT 01-JUN-2010 (TrEMBLrel. 17, Last annotation update)

CHIAL OR CHI.

OS TRIAICOM RESIDENCE OF TRIAICOM.

OC Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; OC Triticeae; Triticom.

OX NCSI_TAXID-4565;

RN [1]

RN [1]

RN [1]

RN SEQUENCE FROM N.A.

RC STRAIN-CV. CHINESE SPRING;

RA Liac Y.C., Kreuzaler F., Fischer R., Reisener H.J., Tiburzy R.;

RL Plant Sci. 103-17-187 (1994).

DR RESEP; PASO41; CAR53626.1; -.

DR RESEP; PASO41; CAR53626.1; -.

DR PRESP; PASO41; CAR53626.1; -.

DR PRESP; PASO41; CAR53626.1; -.

DR PRODON; POBO0072; Chitin_binding; 1.

DR PRODON; POBO0072; Chitin_binding; 1.

DR PRODON; POBO0054; CHITIN_BINDING; 1.

DR PROSITE; PRO0076; CHITIN_BINDING; 1.

DR PROSITE; PRO0076; CHITIN_BINDING; 1.

PR SEQUENCE 320 AA; 33602 MW; F258B9DD8EF65E0E CRC64;
```

Query Match 96.1%; Score 1696.5; DB 10; Length 320; Best Local Similarity 95.3%; Pred. No. 1.5e-141; Matches 305; Conservative 9; Mismatches 5; Indels 1; Gaps 1;

2

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KPSSHDVIIGRWSPSGADQAAGRVPGYGVIINIINGGLECGRGQDGRVADRIGFYKRYCD 300
                                                                                                                              Ä.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15; Mismatches
                                                                                                                              320
                                                                                                                                                                                                                                                                                                                                                                              Pfam: PF00187; chitin_binding; 1.
Pfam: PF00182; clyco_bidro_19; 1.
PRINTS; PF00182; clyco_hidro_19; 1.
ProDom: PD000574; Glyco_hidro_19; 1.
SMART: SM00270; ChtBnl: bind; 1.
PROSITE; PS00773; CHTINASE_19_1; 1.
PROSITE; PS00774; CHTINASE_19_2; 1.
PROSITE; PS00076; CHTINASE_19_2; 1.
PROSITE; PS00026; CHITINASE_19_2; 1.
                                                                                                                                                                                                                                                                                                         Du M., Ha S.B.;
Submitted (APR-1997) to the EMBL/Gen
EMBL; AF000966; AAF04454.1; -.
HSSP; P23951; 2BAA.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Glyco_hydro_19.
                                                                                                                                                                                                               Poa pratensis (Kentucky bluegrass).
                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90.5%;
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                                                          LLGVSYGHNLDCYNQRPFA 318
                                              LLGVSYGDNLDCYNQRPFA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 90.33
Matches 288; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=GLADE;
                                                                                                                                                                                                                                                            NCBI_TaxID=4545;
                                                                                                                                                   01-MAY-2000 (
01-MAY-2000 (
01-JUN-2001 (
CHITINASE.
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Q9SQL3;
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 241
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                                               119
                                                                                            179
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                                                                                                                                                                                      PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=20532799; PubMed=11060301;
Yeh S., Moffatt B., Griffith M., Xiong F., Yang D.S.C., Wiseman S.B.,
Sarhan F., Danyluk J., Xue Y.Q., Hew C.L., Doherty-Kirby A.,
Lajoie G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
31.7 KDA CLASS I ENDOCHITINASE-ANTIFREEZE PROTEIN PRECURSOR.
Secale cereale (Fye).
Enkaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta: Liliopsida: Poales; Poaceae; Pooideae; NCBL_TAXID-4550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MRGVVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
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                MEGVVVVAMLABABFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGSTSDYCGNGCQSQCN
                                                             ìn
                                               GCS-GGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSG
                                                                                             FATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQW
                                                                                                                                            PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
  MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Chitinase genes responsive to cold encode antifreeze proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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BA685E1DB7A58E63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 94.9%; Score 1675.5; DB 10; Best Local Similarity 94.7%; Pred. No. 1.1e-139; Matches 302; Conservative 9; Mismatches 7; In
                                                                                                                                                                                                                                                                                                                         A.
                                                                                                                                                                                                                                                                                                                        318
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EMBL; AF280437; AAG53609.1; -.
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33636 MW;
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                                                                                                                                                                                                                                                   DELGVIYGDNEDCYNQRPFA 320
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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SIGNAL
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PKPSSHDVIIGRWSPSGADQAAGRVPGYGVIINIINGGLECGRGQDGRVADRIGFYKRYC 299
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
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140 KPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDARVADRIGFYKRYCD
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                                                                                                                                                                                                                                (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1597; DB 10;
Pred. No. 8.8e-133;
5; Mismatches 14;
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298 YCDLLGVSYGDNLDCYNQRPFA 319
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                                                                                                                                                                                                                                           321 AA; 33641 MW;
                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 78.9%
Matches 254; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN=NIPPONBARE;
                                                  Triticeae; Secale.
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4530;
SEED CHITINASE-A.
                                                            NCBI_TaxID=4550;
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                                                                                                                                                                                                                                           SEQUENCE
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Q42993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 FAITGSIDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQERGAISDYCTPSSQW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGR--VADRIGFYKR 297
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                                                                                                                Eukaryota, Viridiplantãe, Střeptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae,
                                                                                                                                                                                                                                                                                                                                                                                                                 4;
                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                          Du M., Ha S.B.;
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; AF000964; AAF04453.1; -.
HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                 PROSTIE; PS0773; CHITINASE_19_1; 1.
PROSTIE; PS00774; CHITINASE_19_2; 1.
PROSTIE; PS0026; CHITIN_BINDING; 1.
Chitin-binding.
SEQUENCE 340 AA; 36011 MW; 3613D7059A871E94 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                         Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                         88.2%; Score 1557; DB 10;
llarity 87.9%; Pred. No. 3.1e-129;
Conservative 17; Mismatches 18;
                                                                Last sequence update)
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                                340 AA
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                                                                                                                                                                                                                                InterPro; IPR001002; Chitin_bind.
InterPro; IPR000102; Glyco_hydro_19.
Pfam; PF00187; Chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDNG.
PRODOM; PD0000543; Glyco_hydro_19; 1.
ProDom; PD000609; Chitin_bind; 1.
                                                      Created)
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                                                                                                         Poa pratensis (Kentucky bluegrass).
                                 PRT;
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                                                     13,
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                                                               01-MAY-2000 (TrEMBLrel. 01-JUN-2001 (TrEMBLrel.
                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                         SMART; SM00270; ChtBD1;
                                                    01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                  NCBI_TaxID=4545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
01-MAR-2001
01-JUN-2001
                                                                                                                                                                                  STRAIN=GLADE
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Simi
Matches 282;
                                                                                                                                        Poa.
                                                                                     CHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FRV1;
                                            Q9SQL4;
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                                                                                                                                         Poeae;
                                Q9SQL4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 1
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                      29SQL4
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118 SGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSS 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Secale cereale (Rye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (Tremblrel. 01, Created)
01-NOV-1996 (Tremblrel. 01, Last sequence update)
01-UN-2001 (Tremblrel. 17, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14) (CHIODEXTRINASE) (1,4-BETA-POLY-N-ACETYLEGUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
CHIAL OR CHT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWHTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 321;
                                                                                                                                                                                 Ohnuma T., Yamagami T., Ishiguro M.;
Cloning and Sequencing of the Rye Seed Chitinase.";
E. Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; ABO51578; BAB18519.1; -..
R InterPro: IPR001002; Chitin_bind.
R InterPro: IPR000726; Glitcin_bind.
R Pfam; PF00182; Glyco_hydro_19.
R Pfam; PF00182; Glyco_hydro_19; 1.
R Pfam; PF00182; Glyco_hydro_19; 1.
R Probom; PD000574; Glyco_hydro_19; 1.
R Probom; PD000509; Chitin_bind; 1.
R SMART; SM00270; ChtBD1; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80.5%; Score 1421; DB 10; Length 78.9%; Pred. No. 2.8e-117; cive 29; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76E5902BBC337C8E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00026; CHITIN_BINDING; 1.
Chitin-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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MEDLINE-94049667; PubMed-7901749;
Nishizawa Y., Kishimoto N., Saito A., Hibi T.;
"Sequence variation, differential expression and chromosomal location
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 ATIGSTDVKKREVAAFLAQTSHETIGGWPTAPDGPYSWGYCFNQE-RGAISDYCTPSSQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 PCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 PKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYC
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENDOCHITINASE.
D7331BF4A6B592E3 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 1), Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE)
ACETYLGLUCOSAMINIDASE) (POLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                   of rice chithase genes.";

Mol. Gen. Genet. 241:1-10(1993).

EMBL: D16223; BAA03751.1;

HSSP; PA23951; BAA03751.1;

HSSP; PA23951; BAA03751.1;

Mendel: 1582; Oryas;Chial,1582.

InterPro: IPR001002; Chitin_bind.

InterPro: IPR001002; Chitin_bind.

Pfam; PP00183; Glyco_hydro_19.

Pfam; PP00183; Glyco_hydro_19.

PFNNTS; PR00451; CHTINENDNG.

ProDom; PD000609; Chitin_bind; 1.

PROSITE; PS00773; CHITINASE_19.1; 1.

PROSITE; PS00773; CHITINASE_19.1; 1.

PROSITE; PS00773; CHITINASE_19.1; 1.

PROSITE; PS00774; CHITINASE_19.1; 1.

PROSITE; PS00774; CHITINASE_19.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1352.5; DB 10;
Pred. No. 3e-111;
...-+rhes 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33681 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76.6%;
75.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 DMLGVSYGDNLDCYNQRPY 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 241; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          320 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                   STRAIN-NIPPONBARE;
                                            NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHIA1 OR CHT-2
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Q43294;
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MEDLINE=94049667; PubMed=7901749; Nishikawa Y., Kishimoto N., Saito A., Hibi T.; Nishikawa Y., Kishimoto N., Saito A., Hibi T.; "Sequence variation, differential expression and chromosomal location of rice chitinase genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G-CSGGTPVPVPTPSGG---GVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 FSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--SDYCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        175 PSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFW 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Gaps
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01-NOV-1996 (TLEMBLrel. 01, Last sequence update)
01-NOV-1996 (TLEMBLrel. 17, Last annotation update)
01-JUN-2001 (TLEMBLrel. 17, Last annotation update)
ENDOCHITINASE PRECURSOR (EC 3.2.1.14).
CHIA1 OR CHI-3.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRALAVVVVATAFAVVAVRGEQCGSQAGGALCPNCLCCSQYGWCGSTSAYCGSGCQSQCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; Length 323;
                                                                                                                                                                                                                                      OF THE 1,4-BETA-LINKAGES OF OF CHITIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1C85B6227A33EB06 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.0%; Score 1359.5; DB 10
75.6%; Pred. No. 7.3e-112;
tive 27; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00773; CHITINASE 19_1; 1.
PROSITE; PS00774; CHITINASE 19_2; 1.
PROSITE; PS00026; CHITIN_BINDING; 1.
Chitin-binding; Glycosidase; Hydrolase; Signal.
SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENDOCHITINASE
                                                                                                                                                          STRAIN=CV. INPPONBARE,
Nishizawa Y., Hibi T.;
Plant SCI. 76:211-218(191).
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF TACTIVITY: HYDROLYSIS OF TACTIVITY: HYDROLYSIS OF TACTIVITY: HYDROLYSIS OF TACTIVITY: HYDROLYSIS OF THE BMBL; N56063; CAA39555.1;
-- EMBL; N56063; CAA39555.1;
-- HSSP; P23951; 2BAA.
Mendel; 14776; Orysa; Chial; 14776.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00102; Chitin_bind.
InterPro; IPR00187; chitin_bindi.
IPR00187; CHITINBIRDNG.
PRODOM; PD000654; Glyco_hydro_19; IPR0DOM; PD000654; Glyco_hydro_19; IPRODOM; PD000609; Chitin_bind; IPROCOM; CHITIN_BIND,
IPROCOM; CHITIN_BIND,
IPROCOM; CHITIN_BIND,
IPROCOM; CHITIN_BIND,
IPROCOM; CHITIN_BIND,
IPROCOM; CHITIN_BIND, INTERPROCOM; CHITIN, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295 YKRYCDLLGVSYGDNLDCYNQRPF 318
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                                                                                             Mol. Gen. Genet. 241:1-10(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33764 MW;
                                                                                                                                           SEQUENCE OF 21-323 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 75.6
Matches 245; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA;
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Q42994
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7

Gaps 9

3;

Length 320;

(1,4-BETA-POLY-N-

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spermatophyta; Magnoliophyta; Laurales; Lauraceae; Persea
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                                                                                                                                                                        26 326 E
326 AA; 34586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                     SYGSNLDCYNORSF 315
                                                                                                                                                                                                                                                                                                                                                                              SYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Triticeae; Horder
NCBI_TaxID=4513;
[1]
                      SEQUENCE FROM N.A.
       NCBI_TaxID=3435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHIA1 OR CHI33
                                                                                                                                                                                                             Best Local Sim
Matches 230;
                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                     Query Match
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Q42839;
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                                         GGTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFAIT 123
                                                                                                                                                                                                                                                         1; Gaps
                                                                                                                                                                                                                                                                      4 VVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCS 63
                                                                                                                                                                                                                                                                              16 LVALAVLAAALATAARAEQCGAQAGGARCPNCLCCSRWGWCGTTSDFCGDGCQSQCSGC- 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                            124 GSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAP
                                                                                                                                                                                                                                                                                                                                                                  GKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPS
                                                                                                                                                                                                                                         74.6%; Score 1317.5; DB 10; Length 340; 72.4%; Pred. No. 3.8e-108; Live 36; Mismatches 50; Indels 1;
                                                                                                                                                                                                                      642F13E3928CA7BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
3.2.1.14).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 AA
                                                                                                                                                                                                                CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                               STRAIN=JAPONICA, CV. NIPPONBARE;
MEDLINE=94049667; Pubmed=7901749;
                                                                                                                                                                                                                      340 AA; 35586 MW;
    Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1997 (TrEMBLrel. 03, 01-MAY-1998 (TrEMBLrel. 07, 01-JUN-2001 (TrEMBLrel. 17, CHIALORITINASE PRECURSOR (EC CHIAL OR CHII.
                                                                                                                                                                                                                                            Query Match 74.6%
Best Local Similarity 72.4%
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   304 VSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                   315 IGTGGNLDCYNORPF 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                340
                         SEQUENCE FROM N.A.
           NCBI_TaxID=4530;
                                                                                                                                                                                                                      SEQUENCE
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P93680;
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P93680
ID P99AC P9
DT 011
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SEQUENCE FROM N. A.

SEQUENCE FROM N. A.

SEQUENCE S. HSIGH L., Krebitz M., Akasawa A., Martin B., Starrett D.,
SOWKA S., HSigh L., Krebitz M., Akasawa A., Martin B., Starrett D.,
SOWKA S., HSigh L., Krebitz M., Akasawa A., Martin B., Starrett D.,
SOWKA S., HSigh L., Scheiner O., Breiteneder H.;
Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; 278202; CAB01591.1; -
RRSP: PO2877; HTFV.
RROPE INFO.00726; Glidin_bind.

RICEPPO: IPRO01002; Chitin_bind.

RRINTS: PRO0187; CHITINAINDNG.
PRODOM: PD000679; Chitin_bind; 1.
RRODOM: PD000679; CHILINAINDNG. 1.
RROSITE; PS00774; CHITINASE. 19.1; 1.
RROSITE; PS00774; CHITINASE. 19.2; 1.
SRARI; SRO0774; CHITINASE. 19.2; 1.
SROO774; CHITINASE. 19.2; 1.
SROO774; CHITINASE. 19.2; 1.
SROO774; CHITINASE. 19.2; 1.
SROO774; CHITINASE. 19.2; 1.
SROO775; CHADI.
STGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 SIDVKKREVAAFLAQISHETIGGWPIAPDGPYSWGYCFNQERGAISDYCIPSSQWPCAPG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCDLLGV 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65 GTPVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATIG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hordeum vulgare (Barley).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LILLLLVGLLAGEAFAEQCGRQAGGALCPGGLCCSQFGWCGSTSDYCGPTCQSQCGGV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TIEMBLEEL. 01, Created)
01-NOV-1996 (TIEMBLEEL. 01, Last sequence update)
01-UJW-2001 (TIEMBLEEL. 17, Last annotation update)
CHITIMASE (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENDOCHITINASE.
643B20589E062E61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 73.2%; Score 1305; DB 10 Similarity 73.2%; Pred. No. 4.6e-107 30; Conservative 35; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    332 AA
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248 KPSCHDVITGQWTPSSGDIAAGRVPGYGVIINIINGGLECGFGPDDRVANRIGFYQRYCD 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (1,4-BETA-POLY-N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa (Rice).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoldeae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 KPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYKRYCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 VAMLAAAFAVSAH--AEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCNGCSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTPVPVPTPSGGG-----VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGF
                                                                           Ł
                                                                           G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 333;
SEQUENCE FROM N.A.
STRAIN=IR36; TISSUE=ETIOLATED LEAF;
YUN C.H., Kim J.K., Park Y.H.;
Submitted (NOV-1294) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES GENEL, L37289; AASI377.1,
-HSSP; P23951; ZBAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       E2B65D4155B8C73D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U1-NOV-1996 (TrEMBLE). 01, Last sequence update) 01-7UN-2010 (TrEMBLE). 01, Last sequence update) 01-8HINASE PRECURSOR (EC 3.2.1.14) (CHITOBETRINASE) ACETYLGLUCOSAMINIDASE) (FOLY-BETA-GLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72.5%; Score 1279; DB 10; 71.7%; Pred. No. 9.2e-105;
                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Chitin-binding; Glycosidase; Hydrolase; SIGNAL 1 23 POFFNTTAT.
                                                                                                                                               Mendel; 26; Orysa; Chial; 26.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001025; Glyco_hydro_19.
Ffam; PF00187; Chitin_binding; I.
Pfam; PF00182; Glyco_hydro_19; I.
ProDom; PR00674; CHITINBINNG.
ProDom; PD000609; Chitin_bind; I.
PROSITE; PS00773; CHITINASE 19_1; I.
PROSITE; PS00774; CHITINASE 19_1; I.
PROSITE; PS00774; CHITINASE 19_2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                       CHITINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                       34336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 LLGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                308 VLGIGYGSNLDCYDQRPF 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN=IR36; TISSUE=LEAF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                       333 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Simi
Matches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            042995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CHTILNASE PRECURSOR (EC 3.2.1.14) (CHITODEXTRINASE) (1,4-BETA-POLY-N-ACETYLGLUCOSAMINIDASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCOSOCNGCSGGTPVPVPTPSGGGVSSIISQSLFDQMLLHRN---DAACLAKGFYNYGAF 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VAAANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATS 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.

NCBL_TaxID=4530;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DYCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MRG-----VVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAAAATEPAFGTIGSTETRKQEVAAFFGQTSHETTGGWATAPDGPYSWGYCYRRELGSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.2%; Score 1291.5; DB 10; Length 332; 71.6%; Pred. No. 7.3e-106; Live 33; Mismatches 43; Indels 17;
                                                                                                                                                         OF.
                                                                                                   Identification of an enhancer/silencer sequence directing the
                                                           Leah R., Skriver K., Knudsen S., Ruud-Hansen J., Raikhel N.V.,
                                                                                                                                                   AGENTAL OCCUPATION: HYDROLYSIS OF THE 1,4-BETA-LINKAGES (AGENTAL-D-GLUCOSAMINE POLYMERS OF CHITIN.

MENGL, 134211, AAA5787.1;
HSSP, P23951, 2BAA.
Mendel, 1565, Horvu, Chial, 1565.
InterPro, IPR001022, Chitin, bind.
InterPro, IPR001022, Chitin, bind.
InterPro, IPR001022, Chitin, bind.
InterPro, IPR001022, Chitin, Dind.
Pfam, PF00182, Glyco_hydro_19.
PFam; PF00182; Glyco_hydro_19;
PRINTS; PR00451; CHITINBINDNG.
                                                                                                               aleurone-specific expression of a barley chitinase gene.".
Plant J. 6:579-589(1994).
                                                                                                                                                                                                                                                                                                                                         Prodom; PRO00554; Glyco_lydroc_l9; 1.
Prodom; PD000659; Chitin_bind; 1.
SWART; SW00270; ChEDI; 1.
PROSITE; PS00773; CHITINASE_19_1; UNKNOWN_1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
Chitin-binding; Glycosidase; Hydroclase,
SEQUENCE 332 AA; 35369 MW; 1B33654F49AC9E0F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    333 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIGEYKRYCDLLGVSYGDNLDCYNQRPF 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                           MEDLINE=95078949; PubMed=7987416;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 235; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  042992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Query Match 72.1
Best Local Similarity 73.0
Matches 235; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
   HSSP; P23951; 2BAA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC CHITINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  041180;
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Q41180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDYCTPSSQWPCAPGKKYFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKT 229
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Spermatophyta; Magnoliophyta, Liliopsida, Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MEDLINE-96189256; PubMed=8605293;
Xu Y., Zhu Q., Panbangred W., Shirasu K., Lamb C.;
"Regulation, expression and function of a new basic chitinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 AAANSFSGFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--
                                                                                           rice (Oryza sativa L.).",

plant Mol. Biol. 30:387-401(1996).

-!-CATALYTIC ACTIVITY: HYDROLYSIS OF THE 1,4-BETA-LINKAGES OF N

ACETYL-D-GLOCOSMINE POLYMERS OF CHITIN.

R MSD; X87109; CAA60590.1; -.

R MSD; P293951; EBAA.

R InterPro; IPR001002; Chitin_bind.

R InterPro; IPR001002; Chitin_bind.

R InterPro; IPR0012; Chitin_bind.

R Pfam; PF00187; chitin_binding.

R Promom; PF00187; Glyco_hydro_19; 1.

R PRINTS; PR00451; CHITIBINDNG.

R PRODOM; PD000699; Chitin_bind; 1.

R SMART; SM00270; ChtBD1: 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 322 AA; 34505 MW; AD56FE9CF7D99B09 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.2%; Score 1274; DB 10; 70.8%; Pred. No. 2.4e-104; tive 28; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chitin-binding; Glycosidase; Hydrolase; Signal.
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Biosci. Biotechnol. Biochem. 0:0-0(1994).
EMBL; Z29961; CAA82849:1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     290 DRIGEYKRYCDLLGVSYGDNLDCYNQRPF 318
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01-NOV-1996 (TrEMBLrel. 01, Last seq
01-UNN-2001 (TrEMBLrel. 17, Last ann
CHITINASE CLASS I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00774; CHITINASE_19_2; 1. PROSITE; PS00026; CHITIN_BINDING; 1.
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Best Local Similarity 70.89
Matches 233; Conservative
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GFATTGSTDVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGAT--SDYCTPS 176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GSCGGGADPA---SGGASGVASIVSRSLFDQMLLHRNDAACPAKNFYTYDAFVAAANAYP 117
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Neale A.D., Wahleithner J.A., Lund M., Bonnett H.T., Kelly A.,
Neale A.D., Wahleithner J.A., Lund M., Bonnett H.T., Kelly A.,
Meeks-Wagner D.R., Peacock W.J., Dennis E.S.;
Meeks-Wagner D.R., and extensin are expressed :
"Chitinase, beta-1,3 -quadranse, osmotin, and extensin are expressed :
tobacco explants during flower formation.";
Plant Cell 2.673-684(1990).
BEMBL: S44869; AAB23374.1;
HSSP; P23951; 2BAA.
Mendel: 14770, Nacta; Chial; 14770.
Interpro; IPR001002; Chitin, bind.
Interpro; IPR000726; Glyco_hydro_19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTGCQSQCN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIINGGLECGRGQDGRVADRIGFYK
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Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                     Chitin-binding.
SEQUENCE 319 AA; 33600 MW; C990572C114FC0A9 CRC64;
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Mendel; 1578, Orysa; Chial; 1578.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001002; Chitin_bind.
InterPro; IPR001705; Glyco_hydro_19.
Ffam; PF00182; Glyco_hydro_19; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHITINBINDIG.
ProDom; PD000659; Chitin_bind; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00773; CHITINASE_19_1; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
PROSITE; PS00774; CHITINASE_19_2; 1.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Vitaceae;
Vitis.
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                                                                                                                                                                                                                                                                                                                                                                               127 DVKKREVAAFLAQTSHETTGGWPTAPDGPYSWGYCFNQERGATSDYCTPSSQWPCAPGKK 186
                                                                                                                                                                                                                                                                                                                                                                                                67 PVPVPTPSGGGVSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFSGFATTGST 126
                                                                                                                                                                                                                                                                                                                                       89
                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular characterization of Vitis vinifera genes encoding chitinases differentially expressed in berries and leaves infected benitianal pathogens.";
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ291506; CAC14015.1; -.
InterPro; IPR001002; Chitin.bind.
InterPro; IPR00102; Chitin.bind.
Pfam; PF00182; Chitin.bind.
Pfam; PF00182; Chitin.binding; 1.
Pfam; PF00182; Chitin.binding; 1.
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Propon; PD000574; CHITINBINDNG.
Probom; PD000574; Glyco_hydro_l9; 1.
SMART; SM00270; ChtBDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 YFGRGPIQISHNYNYGPCGRAIGVDLINNPDLVATDPVISFKSALWFWMTPQSPKPSCHD
                                                                                                                                                                                                                                                                          187 YFGRGPIQISHNYNYGPAGQAIGTDLLNNPDLVASDATVSFKTALWFWMTPQSPKPSSHD
                                                                                                                                                                                                                                                          8 AMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFCGTTSDYCGTG-CQSQCNGCSGGT
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STRAN=CV. UGNI BLANC; TISSUE=LEAF;
RODETT N., Roche K., Lebeau Y., Breda C., Boulay M., Esnault Buffard D.;
                                                                                                                                                                                                 Length 328;
                                                                                                                                                                                                                            Indels
                                                                                                                                                    328 AA; 35300 MW; F687A32555D9DB55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-UNA-2001 (TrEMBLrel. 17, Last annotation update)
CHITINASE PRECURSOR (EC 3.2.1.14).
                                                                                                                                                                                              Query Match 71.4%; Score 1260; DB 10; Best Local Similarity 71.8%; Pred. No. 4.3e-103; Matches 224; Conservative 31; Mismatches 53;
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Pfam; PF00187; chitin_binding; 1.
Pfam; PF00182; Glyco_hydro_19; 1.
PRINTS; PR00451; CHTIINBINDNG.
PTODOM; PD0000574; Glyco_hydro_19; 1.
PROSITE; SW00270; ChtED1; 1.
PROSITE; PS00773; CHTIINASE_19_1; 1.
PROSITE; PS00774; CHTIINASE_19_2; 1.
PROSITE; PS00774; CHTIINASE_19_2; 1.
Chitin-binding.
SEQUENCE 328 AA; 35300 MW; F687A325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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3, 2002, 18:47:02

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65 GTP----VPVPTPSGGG--VSSIISQSLFDQMLLHRNDAACLAKGFYNYGAFVAAANSFS 118
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                                                                                                                                                                                                                 12;
                                                                                                                                                                 Length 325;
                                                                                                                                                                                                                 Indels
                                                                    CHITINASE, 05DE2B9575ABEAD8 CRC64;
                                                                                                                                                              71.2%; Score 1256; DB 10;
68.5%; Pred. No. 9.5e-103;
Live 41; Mismatches 48;
PROSITE; PSO0026; CHITIN_BINDING; 1.
Chitin-binding; Glycosidase; Hydrolase; PGGNAL
1 22 POTENTIAL.
CHAIN
SEQUENCE 325 AA; 34631 MW; 05DE2B957.
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                                                                                                                                                                      Query Match
Best Local Similarity 68.5
Matches 220; Conservative
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3, 2002, 14:21:51; Search time 3990.51 Seconds (without alignments) 3187.393 Million cell updates/sec
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771
1 atggcgaggtttgctgccct......agaggaacttcgctagctag
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                      1472140 seqs, 8248589755 residues
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Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
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Perfect score:
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                                                                         Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	X78671 H.vullgare m A778672 H.vullgare m A127626 Hordeum v A127626 Hordeum v AB016497 Orgza sativ AF001500 Orgza sativ AF000965 Poa prate AF000965 Poa prate AF000965 Poa prate AF000965 Poa prate X76041 T.aestivum 184465 Sequence 2 D16223 Rice Cht.3 AP003685 Orgza sati 134211 Hordeum vul M62904 H.vulgare E AR02754 Sequence 9 134210 Hordeum vul M62904 H.vulgare C AR051578 Secale ce AF000964 Poa prate AF000964 Poa prate AF000964 Poa prate AF000964 Poa sativ X56063 O.sativa mR D16221 Rice Cht.1 AB051578 Secale ce AF000964 Poa prate AF01578 Secale ce AF000964 Poa prate AF01578 Secale ce AF000964 Orga sativ X54360 Orga sativ X6063 O.sativa RC AR01388 Tobracco pat AR01588 Sequence AR01782 Sequence AR01781 Sequence AR01781 Sequence AR057485 Sequence AR057485 Sequence AR057485 Sequence	PLN 01-NOV-1994 Embryophyta; Tracheophyta; ; Poales; Poaceae; Gummesson, P.O., Kragh, K. sequence of a basic lery mildew
QI	HVCHT2A HVCHT2A HVCHT2B AR280438 HVU276226 AR016497 OSAF001500 SILCCHTA AR000966 FACCHIG RICCHTA AF000966 FACCHIG RICCHTA AF000966 FACCHIG RICCHTA AF000966 AR003685 BLXCH13AA BLXCH13AA BLXCH13AA AF000964 AF000966 AF0009666 AF000	HYCHTZA 1028 bp mRNA PLN N H.vulgare mRNA for chitinase 2a. X78671. X78671.1 GI:563486 chitinase. barley. M Hordeum vulgare Bukaryota; Viridiplantae; Streptophyta; Embryoph; Spermatophyta: Magnoliophyta; Liliopsida; Poales; Pooldeae; Triticeae; Hordeum. I (bases 1 to 1028) Bryngelsson, T., Collinge, D.B., Green, B., Gummesse and Thordal-Christensen, H. Purification, characterization and cDNA sequence chitinase from barely infected with powdery milded Unpublished I (bases 1 to 1028) Bryngelsson, T.L. Sequence chitinase from barely infected with powdery milded bryngelsson, T.L.
ingth DB	11028 8 8900 8 8900 8 90013 8 90013 8 90013 8 90013 8 90013 8 900 8 90013 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 900 8 90	1028 bg IRNA for c II:563486 II:563486 Gare Myridipli Vari Magno Triticeae: To 1028 To 1028 I to 1028 I to 1028 I to 1028
Query Match Len	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	HYCHT2A H.Vulgare ME X78671.1 Chitinase. Chitinase. Darley. Hordeum vulc Bardeyca; V Bordeae; Tr Pooldeae; Tr Pooldeae; Tr Pooldeae; Tr Pooldeae; Tr Pooldeae; Tr Chases 1 Bryngelsson and Thordal chitinase fi Chases 1 Bryngelsson and Thordal
Score	11	HYCHTA LOCUS DECINITION H DEFINITION X ACCESSION X VERSION X VERSION X VERSION X VERSION X VERSION X VERSION X VERSION X ACCESSION X VERSION X SOURCE DE PROPERSION DE PROPERSION DE PROPERSION DE PROPERSION DE COURNAL OF COURT OF
Result No.	0 111111111111111111111111111111111111	RESULT 1 HVCHT2A LOCUS DOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL REFERENCE AUTHORS

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539 GIGTCCTTCAGGACGCCGAIGTGGTTCTGGATGACGCCCAGGGCAACAAGCCGTCGAGC
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H.vulgare mRNA for chitinase
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GRNDANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS"
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              Department of Plant of Agricultural Sciences,
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Pred. No. 9.4e-88;
0; Mismatches 37;
              Submitted (16-MAR-1994) T.L. Bryngelsson,
Breeding Research, The Swedish University
S-268 31 Svaloev, SWEDEN
Location/Qualifiers
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TVINFWHTAGONKDSSHIVALGSWTPTRADFAAGFARTGKTVHIINGGLECGWGQND
ANVDRIGYYTRYCGMLGTATGGNLDCYTQRNFAS"
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2 (bases to 1013)
2 (bases) T.L.
Bryngelsson, T.L.
Direct Submission
Direct (16-MAR-1994) T.L. Bryngelsson, Department of Plant
Breeding Research, The Swedish University of Agricultural Sciences, 9-268 31 Svaloev, SWEDEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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Bryngelsson, T., Collinge, D.B., Green, B., Gummesson, P.O., Kragh, K. and Thordal-Christensen, H. Purification, characterization and cDNA sequence of a basic chitinase from barely infected with powdery mildew
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56.814
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Secale cereale 24.8 KDa class II endochitinase-antifreeze protein
precursor, mRNA, complete cds.
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Length 1013;
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   Hew, C.L.
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Yeh,S., Moffatt,B., Griffith,M., Xiong,F. and Hew Direct Submission
Submitted (20-JUN-2000) Biology, University of Wai University Ave West, Waterloo, ON NZL 361, Canada
Sarhan, F., Danyluk, J., Xue, Y.Q.,
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ilarity 92.8%; Pred. No. 6e-80;
Conservative 0; Mismatches 53;
                                                                                                                                      (2000)
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                                                                                                             winter cereals
Plant Physiol. 124 (3), 1251-1264
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Itoh,Y., Yamamoto,K. and Sasaki,T.
Direct Submission
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AJ276226 AJ276226.1 GI:9501333 Chitinase; cht2 gene; pathogenesis-related protein 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MLRSPRSCSPWRWAAPRRRAWAPSSRNRCYASMLPNRDNSQCPG
GOYTYVFTATAAANIPPGFGTTGSADOVRRELAAFFGGTSHETTGGTRGAADQFGWGY
CFKEBINKATSPPYGRGPIQLFGGSNYDLAGRAIGKDLVSNPDLVSTDAVYSFRTAI
WFWMTAGNRESSHWYALGRWFPTAADTAAGRYPGYGVITUTINGGLECGMGQNDANV
DRIGYYTRYCGMLGTATGGNLDCYTQRNFAS"
                                                                                                                                                                                                                                                                                                                                               Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
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Submitted (20-JUL-2000) M. Bevan, John Innes Centre, Norwich, NR4
7UH, United Kingdom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in barley during
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                                                                  ggccgccgacaccgctgccggcagggtacccggatacggagtgatcaccaatatcatcaa
              cggcgggctcgagtgcggaatgggccggaacgacgccaacgtcgaccgcatcggctacta
                                                                                                       cacgogotactgoggcatgotcggcacggcaccggaggcaacctcgactgotacaccca
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ilarity 92.2%; Pred. No. 1.4e-77;
Conservative 0; Mismatches 57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
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/db_xref="taxon:4513"
/country="United Kingdom"
/dev_stage="leaf"
/clone="d6"
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/gene="cht2"
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/protein_id="CAB99486.1"
/db_xref="G1:9501334"
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Green, R.M. and Bevan, M.
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                                                                                                                                                              gaggaacttcgctagctag 771
                                                                                                                                                                         /gene="cht2"
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Green, R.M.
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Embryophyta; Tracheophyta; Submitted (22-JUL-1998) to the DDBJ/EMBL/GenBank databases. Yoshifumi Itoh, National Food Research Institute, Applied Microbiology; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8642, Japan (E-mail:1908:ifumi@nir.affrc.go.jp, Tel:+81-298-38-8075, 01-AUG-1998 Oryza sativa Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza. AB016497 923 bp mRNA PLN
Oryza sativa mRNA for chitinase, complete cds.
AB016497
GL:3370779
chitinase; chitinase IIa.
Oryza sativa cDNA to mRNA.

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/protein_id="AAB58238.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4530"
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79.2%;
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STDAVVSFKTAIWFWMTAQGNKPSCHDVILGRWTPSAAEHAAGRVPGYGVITNIINGG
IECGYGQNDANVDRIGYYKRYCDMLGAGYGSNLDCYNQRNFAS"
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                                                                                                                                                                                                                                /trānslation="mttttrfrvolaacaaasllavaasgaaaggvgsvitoavfnsm
LPNRDNSQCPARGFYTYDAFIAAANSFPAFGTSGGSAELIRRELAAFFGQTSHETTGG
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2 (bases 1 to 923)
Itch,Y., Yamamoto,K. and Sasaki,P.
Nucleotide sequence of rice acidic class II chiitinase OsChia2a
Published Only in Database (1998) In press
Location/Qualifiers
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83.6%; Pred. No. 4e-
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                                                               1. .923
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903. .908
                                                                                                                                                                                                                                                                                                                                                              /note="19 a nucleotides"
294 c 277 q 16
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7. .792
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2 (bases 1 to 913)
Yun, C.-H., Lee, M.-C., Lee, J.S., Yun, K.J. and Bun, M.Y.
Direct Submission
Submitted (29-APR-1997) Dept. of Cytogenetics, National Institute of Agricultural Science and Technology, RDA, Seodundong, Suweon 441-707, Korea DNSQCPATGFYTSSAFIAAANSFRRSARAGGAPSSSRRELAAFFGQTSHETTGGTRGS
SDOCGWGYCTCKEBINGATSPPYTGGFPIQLTGGSNYQAAGNALALDLYGNPDLYSTDA
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza,
I (bases 1 to 913)
Yun, C. H., Lee, M. C., Lee, J. S., Yun, K. J. and Eun, M. Y.
Isolation and characterization of a rice chitinase cDNA clone from rice blast fungus-infected rice leaves 678 717 738 TGGCG-----GCGGCAGGGCGTCGGTCATCACGCAGGCGGTTTCAACAGCAIG 121 618 657 597 Gaps OSAF001500 913 bp mRNA PLN 22-MAY-1997 Oryza sativa clone MIRCH1 chitinase mRNA, partial cds. AF001500 12 ACGCCGAGGTITGTTCAGCCTTGCCGTGC----CGGCGCGCCTGCTCGCCGTGGCGGCA 67 538 tgccacaacgtcgccctacgccgctggacgccgacggccgccgacaccgctgccggcagg cggaacgacgccaacgtcgaccgcatcggctactacacgcgctactgcggcatgctcggc 559 TGCCACGACGTCATCCTCGGCCGGTGGACGCCGTCGGCGGCGGCGGAACACGCCGCCGCCGC 598 gtacccggatacggagtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggc 739 GCAGGCTACGGCAGCAACCTCGACTACAACCAGCGCAACTTCGCCAGCTAG 792 718 acggecaccggaggeaacctegactgetacacceagaggaacttegetagetag 771 13; /dev_stage="seedling" /tissue_type="blast fungus-infected leaves" /clone="MIRCH1" Length Indels 0; Mismatches 146; DB 8; Score 474.4; DB 8 Pred. No. 1.4e-55; 161 t

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/product="chitinase"
//protein_id="aAC37516.1"
//db_xxef="c1:2440043"
//translation="ELAAFEGCTSHETTGGTRGSSDOFOWGYCFKEEINKATSPPYYG
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ILGRWIPSAADTAAXTVPGYDGTTNIINGGIEGGVGONDANVDRIGYYKRYCDMLGTG
YGSNLDCYNQRNFAA
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a; Poales; Poaceae;
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Oryza sativa.
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Spermatophyta; Magnoliophyta; Liliopsida; Poales
Enrhartoideae; Oryzaee; Oryza.
1 (bases 1 to 1186)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLN
                                                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                Score 395.2; DB 8
Pred. No. 8.6e-45;
0; Mismatches 83
 /note="(vector lambda ZAPII)"
                                                                                                                                                                                             μ
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           <1. .528
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191 c 181
                                        /note="putative"
                                                    /codon_start=1
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Liliopsida; Poales; Poaceae;
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1 (bases 1 to 652)

2 (be, M.S., Choe, M.S., Jeong, S.Y., Lee, S.I., Cheong, Y.H., Lee, S.H., Choi, Y.J., Han, C.D., Kang, K.Y., and Cho, M.J.

2 new class II file chilinase, Rcht2, whose induction by fungal elicitor is abolished by protein phosphatase I and ZA inhibitor 98278381
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 ctgcccaaccgcgacaactcgctgtgcccggccagagggttctacacgtacgacgccttc 180
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chitinase (Rcht2) mRNA, 3' end of
                                                    181 ategeegeegacacetteeegggetteggeaceaceggeageg---eegaegaeate
                                                                 238 aagogogacotogocotttettoggccagacetoccacgagaccacoggagggacgaga
                                                                                                                                                                                                                                      298 ggcgctgccgaccagttccagtggggctactgcttcaaggaagaataagcaaggccacg
                                                                                                                                                                               358 tecceaccatactatggacgggacccatecaattgacagggggggtccaactacgatett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Oryza sativa"
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LHRNDGACPARGFYTYEAFLAAAAFPAFGGTGNTETRKREVAAFLGQTSHETTGGWP
                                                                                                                                                                                                                                                                                                                                                                                  TAPDGPFSWGYCFKQEQNPPSDYCQPSPEWPCAPGRKYYGRGPIQLSFNFNYGPAGRA
IGYDLLSNPDLVATDATVSFKTALWFWMTPQGNKPSSHDVITGRWAPSPADAAAGRAP
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                                                                                                                                                                                                                                                                                                                                           /translation="MSTPRAASLAKKAALVALAVLAAALATAARAEQCGAQAGGARC
                                                                         Direct Submission Submitted (13-NOV-1996) Y. Nishizawa, NATIONAL INSTITUTE OF AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI 305, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518
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Pred. No. 5e-36;
0; Mismatches 219; Indels 42;
         location of rice chitinase genes
Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161
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                                                                                                                                                                                                                                                  10. .1032
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Nishizawa,Y.
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GWCGSTSDYCGDGCQSQCDGCGGGGGGGGGGGGGGGGAVEAVSKELFEQLLLHRN
DAACPARGFYTYDAFVTAAAAFPDFAATGDDEARKREVAAFLGQTSHETTGGWATAPD
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LLNNPELVASDPVVSFKTALWFWMTPQSPKPSCHDVTTGQWTPSSGDIAAGRVPGYGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (strain IR36) seedling etiolated leaf cDNA to mRNA.
Oryza sativa
Dryza sativa
Dryza sativa
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartcideae; Oryzeae; Oryza
1 (bases 1 to 1291)
Yun, C.-H., Kim, J.-K. and Park, Y.-H.
Isolation and Characterization of A Rice Chitinase cDNA
Unpublished (1994)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          818
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-----gocacytccccaccatactatggacggggacccatccaattgacagggcggtc 404
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Oryza sativa chitinase mRNA, complete cds.
1.37289
1.37289:1 GI:561872
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/db_xref="G1:561873"
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/organism="Oryza sativa"
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/EC_number="3.2.1.14"
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/haplotype="2n=24"
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Best Local S:
Matches 507,
                  ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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  LOCUS
DEFINITION
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TITLE
JOURNAL
                                                                                                                                                                                                                                     BASE COUNT
ORIGIN
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/BC_number="3.2.1.14"
/BC_tuntion="chitinolytic activity, antifungal activity"
/evidence=experimental
/product="chitinase"
1291
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                                                                                                       44;
                                                                                       Length 1291;
                                                                                                       Indels
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                                                                                    Score 307.2; DB 8;
Pred. No. 5.2e-33;
0; Mismatches 233;
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                                                                                    39.8%;
ilarity 65.3%;
Conservative
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                                                    394 C
                                                                                             Similarity
                                                   239
                              polya_site
BASE COUNT
ORIGIN
 mat_peptide
                                                                                              Best Lócal Sim
Matches 521;
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RESULT 1 AF000965

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ta; Liliopsida; Poales; Poaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1173;
                                                                                                                                                                                                                  U.C. Berkeley,
 DNA PLN (Chi3) pseudogene sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.3%; Score 302.8; DB 8; 64.5%; Pred. No. 2.1e-32; ive 0; Mismatches 237;
                                                                                                                                               Pooldeae; Poeae; Poa.

1 (bases 1 to 1173)

Du,M. and Ha,S.B.

Direct Submission

Submitted (22-APR-1997) Plant Biology,
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1. 1173
7. 1173
/organism="Poa pratensis"
/strain="Glade" raxon:4545"
/db_xxef="taxon:4545"
/gene="Chi3"
/gene="Chi3"
/gene="Chi3"
/gene="Chi3"
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                                                                                                                               Spermatophyta; Magnoliophyta;
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                                                                                                Poa pratensis
Eukaryota, Viridiplantae,
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AF000965 1173 bp Poa pratensis chitinase AF000965 AF000965.1 GI:6164586
                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/pseudo
                                                                               Kentucky bluegrass.
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507; Conservative
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Liao,Y.C., Kreuzaler,F., Fischer,R., Reisener,H.J. and Tiburzy,R. Characterization of a wheat class Ib chitinase gene differentially induced in isogenic lines by infection with Puccinia graminis Plant Sci. 103, 177-187 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 1985)
              347 ACAACGCCTICATCGCCGCCGCCGCCATTTTCGCGGTTTCGGGACCACGGGCAGCACC 406
                                                              ---ggacgagaggcgctgccgaccagttccagtggggctactgcttcaaggaagataa 346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH,
Worringer Weg, 52056 Aachen, FRG
2 (bases 1 to 1985)
                                            acgacateaagegegectegeegecttetteggeeagaceteeeaegagaceaegag
                                                                                                                   ---aaggccacgtccccaccat
                                                                                                                                                                                                                 368 actatggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagag
                                                                                                                                                                                     428 cgatcgggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtcct
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X76041
X76041
CHI GI:416028
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71. .1595
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/organism="Triticum aestivum"
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/db_xref="taxon:4565"
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CHI gene; endochitinase.
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/gene="CHI"
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GTTSDYCGFGCQSQCNGCSGPTPVTPPSGGGGVSSIVSQSLFEDOMLLHRUDAACLAK
GTTSDYCGFGCQSQCNGCSGPTPVTPPPSGGGGVSSIVSQSLFEDOMLLHRUDAACLAK
GFYTYNNETAAANSFAGFGTFGSTDVRKFEVAAFLAQTSHFTTGGWPTAPDGPVSWGY
CFKQEQGATSDYCSPSGWPCAPGKFYFGRAPLQJSSNAVYGPAGQAIQTDLLNNPDL
VAIDPTVSFKTALMWFWATAQSFKPSSHAVITGQWSSSSADQAAGRVPGYGVITNING
GLECGGGQDNRVADRIGFYKRYCDLLGVSTGNNLDCXSQRPFGS"
366 c 327 g 179 t
                                                                                                                                                                                                                                                                                                                                                                                     Poa pratensis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Poeae; Poa.
1 (bases 1 to 1080)
Du,M. and Ha,S.B.
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                             cgctgccggcagggtacccggatacggagtgatcaccaatatcatcaacggcgggctcga
                                                                                                                                           cggcatgctcggcacggccaccggaggcaacctcgactgctacacccagaggaacttcgc
                                                                                     gtgcggaatgggccggaacgacgccaacgtcgaccgcatcggctactacacgcgctactg
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Submitted (22-APR-1997) Plant Biology,
                                                                                                                                                                                                                                                                                                                       (Chi2) gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pratensis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAF04454.1"
/db_xref="G1:6164588"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       location/Qualiflers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="Glade"
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/organism="Poa
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02-AUG-1996

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39.0%; Score 300.6; DB 6
llarity 65.6%; Pred. No. 4.3e-32;
Conservative 0; Mismatches 214
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Sequence 2 from patent US 5695939,
184465 1 GI:3021985
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409 c 353 g
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                                                                                                                                                        /protein_id="CAA5362".
/db_xref="G1:416029".
/db_xref="G1:416029".
/db_xref="SPTREMBL:041539".
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GSTSDYCGNGCOSQCNGCSGGTPVPVPTPTGGGVS511SQSLPDQMLLHRNDAACA
GSTSDYCGNGCOSQCNGCSGGTPVPVPTPTGGAVSTSTSQSLPDQMLLHRNDACQA
GSTSDYCGNGCOSQCNGCSGGTPVPVPTPTGGAVSTSTSGVSTPTTGGWPTAPDGPYSWG
GSTVNCAFVAANNSFNGCAPGKKYTEGARGPIGTSYNNYGPAGAASDCAASPSWG
LVATDATVSFKTALNFWMTPQSFKFSSHDVITGRWSFSGADQAAGRVPGTYGTLINNPD
GGLECGRGQDGRVAADRIGFYKRYCDLLGVTYGDNLDCYNQRPFA"
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                                                                                                                                                                                                                                                                                                                                                                Score 301.4; DB 8
Pred. No. 2.6e-32;
0; Mismatches 221
                                                                                                                                                                                                                                                                                                     /product="endochitinase"
554 c 552 g 412
                                                                                                                                                /product="endochitinase"
                                                                                                                                      /codon_start=1
                                                             /gene="CHI"
600.
                       250. .254
/gene="CHI"
390. .394
  71. .75
/gene="CHI"
                                                                                                                                                                                                                                                                                                                                                            39.1%;
65.3%;
                                                         /gene="CHI"
529. .536
                                                                                                     /gene="CHI"
633. .1595
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693, 1592
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/gene="CHI'
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2, 04-APR-1998 321 177 Gaps 381 tteategecgeceaacatteeegggetteggeaceaeeggeageggegaegaeate 237 441 294 501 354 561 99acggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgatc 432 621 681 cgccaacgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccac 606 atacggagtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacga 58 geggggggtgccgcgcgcagggcgtcgggtcaggtcatcacggggtcggtgtacgcgagc actotycocaaccycygacaactoyotytycocyyocayayyyttotacacytacyacycc 238 aagegegacetegeegeettetteggeeagaceteecaegagaceeeggag---ggaeg 562 GGGCCGGACTACTGCCAGCAGAGCGCGCAGTGGCCGTGCGCCGCCGCGGAAGAAGTACTAC agaggegetgeegaceagtteeagtgggetactgetteaaggaaggataageaaggee --cccaccatactat elements Length 1151; 1 (bases i to 1151) Zhu,Q. and Lamb,C.J. Plant defense genes and plant defense regulatory Patent: US 5695939-A 2 09-DEC-1997; Location/Qualifiers Indels PAT eggaggeaacetegactgetacacecagaggaaettege 764 214; DB 6;

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Chromosome 6.
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acggccatgtggttctggatgacggcgcagggaaacaagccgtcgtgccacaacgtcgcc
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Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chitinase genes
Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
               ctacgeegetggaegeegaeggeegeegaeaeegetgeeggeagggtaeeeggataegga
                                                                                                    613 gtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgccaac
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae;
Enrhartoideae, Oryzeae, Oryza.
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endochitinase.
Oryza sativa (strain Nipponbare) DNA, clone RCG3.
Oryza sativa
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Rice Cht-3 gene for
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Nishizawa,Y.
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1833. 1846
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/product="endochitinase"
/7 7 7 666
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Tue May

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Sasaki, T., Matsumnoto, T. and Yamamoto, K.

Direct Submission

**Matsumoto, T. and Yamamoto, K.

Direct Submission

**L Submission

**Norm: This is a "working draft" sequence

** Norm: This is a "working draft" sequence

** This Sequence will be replaced

** The accession number will be preserved.

** The accession number will be preserved.
                                                                                                                                                            Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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, *** SEQUENCING IN
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0548E04
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PROGRESS ***, in ordered pieces.
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/organism="Oryza sativa"
/cultivar="Nipponbare"
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141534 bp
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Best Local Similarity 66.1%;
Matches 483; Conservative
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                                                                                                                                              Oryza sativa
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19411 CCGGACCTGGTGGCGTCGGACGCCACCGTCTCAAGACGGCGTTCTGGTTCTGGATG 19352
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		Description	Rye chitinase-like	cDNA encoding a ma	cDNA encoding a ma	RCH10 chitinase ge	Rice chitinase RCH	Rye chitinase-like	Nucleotide sequenc	Sequence encoding	Floral organ-speci	cDNA encoding a ma	PR-Q cDNA cloned i
SUMMARIES		qi	AAX24890	AAA96231	AAA96230	AAQ31408	AAQ81346	AAX24889	AAF54983	AAQ62518	AAV49982	AAA96224	AAQ06185
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		Score	651.2	470.6	327.4	300.6	300.6	299.4	297.4	295.6	262.2	246	239.6
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ALIGNMENTS

	AAX24890 standard; cDNA; 756 BP.		0;		1999 (first entry)		Rye chitinase-like protein CHT46 cDNA clone ch-46.		CHT46; chitinase-like protein; antifreeze protein; AFP;	winter rye; antifungal; fungicide; cold tolerance; irost tolerance;	transgenic plant; preservation; cryopreservation; tumour; tnerapy;			Secale cereale.		Location/Qualifiers	1756	ed :		166		67756	/*tag=== b /note=="sepsarately claim 2"		65-A2.	.1999.	-1998; 98WO-CA00745.	-1997; 97US-0903872.
KESULI I	AAX24890		AAX24890;		21-JUN-1999		Rye chit		CHT46; (winter	transge	ss.		Secale		Key	CDS			sig_peptide		mat_peptide			WO9906565-A2.	11-FEB-1999.	31-JUL-1998;	31-JUL-1997;
KESULII VAVA	2	XX	AC	X	DŢ	XX	DE	X	ΚW	ΚŇ	ΚW	ΚW	XX	SO	X	ĿН	FΤ	FI	FT	Еď	ŁŢ	FT	FT	XX	PN	XX OZ	PF.	XX RA

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etc.

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The present sequence encodes winter rye (Secale cereale L. cv. Muskateer) CHT46 preprotein (see AAM98081). Mature CHT46 (see AAM98081) is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHT46 CDNA (ch-46) was obtained by isolating pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed, and then sorting the cold-induced chitinase CDNAs to determine which encoded proteins with ice-binding ability. CHT46 and CHT9 (see AAM98079-80) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               201 caccaccygcaycacygacytcaaycycyayytcyccyccttcttcygccayacctc 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins can be used: to increase freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression
                                                                                                                                       New nucleic acid encoding antifreeze polypeptides from plants particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 756;
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Pred. No. 1.2e-105;
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92.8%;
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           (ICEB-) ICE BIOTECH INC
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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18899, and AAB18900-015), and glucosyl hydrolase family 18 chitinases (AAB18895, AAB18897-98 and AAB18900-011. The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence
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cDNA encoding a maize chitinase polypeptide designated ZmCh15.
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                                                                                                                                                                                                                                                                             413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18;
                                                                                 tacgogagoactotgoccaaccgogacaactogotgtgoccggocagagggttotacacg 168
                                                                                                                                                 233
                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy pathogen control; disease resistance; molecular marker; ss.
                                                                                                                                                                                                                       tgeggegtgggggaaaacgccgaacgtcgaccgcatcggctactacaagcgctactgc
                                                                                                                                                 tacaaccagatgetgeccaaccgegacaacacgeagtgeceegecaacggettetacaee
                                                                                                                                                                                  aactacgatcttgccgggagagaggtcgggaaggacctggtgagcaacccagacctagtg
                                                                                                                                                                                                                                                                                                                                                               aactaccagcaagccggggacgcgataggcgaggacctggtgaacaacccggacctggtg
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                                                                                                                                                                       tacgacgeetteategeegeegeeacaeetteeegggetteggeaceeeggeagegee
                                                                                                                                                                                                               gacga---catcaagegegacetegeegeettetteggeeagaceteeeagagaceace
                                                                                                                                                                                                                                                         ggaggacgagaggcgctgccgaccagttccagtggggctactgcttcaaggaagagata
                                                                                                                                                                                                                                                                                                  agcaaggccacgtccccaccatactaggacggggacccatccaattgacagggcggtcc
                                                                                                         114 geggegetgetgeteggegtggeggeageggaegtggegtegateateaegeaggaegtg
                                         Length 1013;
                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding a maize chitinase polypeptide designated ZmCh14
                                                              Indels
            G; 190 T; 0 other;
                                         DB 21;
                                                              0; Mismatches 144;
                                         Score 470.6; DB 2
Pred. No. 3.8e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
            278
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            ပ်
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            233 A; 312
                                         61.0%;
79.5%;
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                                                                Conservative
                                           Query Match
Best Local Similarity
            BP;
            Sequence 1013
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                                                                570;
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                                                                Matches
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QΥ q QΥ

g Q q QΥ

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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18895, AAB18897-98 and AAB1800-01). The level of chitinases (AAB18895, AAB18897-98 and AAB1800-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence
                                                                                                                                                                                                                                                                                                                                                                                                          crop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cettetteggecagaceteceaegagaceaeggaggaegaggaggegetgeegaeeagt 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acctgaacctggtggcaacccggacctggtggcgagcgaccccgtggtagccttcaaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
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Pred. No. 3.7e-49;
0; Mismatches 246;
                  "chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 82-83; 96pp; English.
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Best Local Similarity 66.5
Matches 501; Conservative
                    /product=
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  /*tag=
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                                                            WO200056908-A2
                                                                                                                                                09-MAR-2000;
                                                                                                                                                                                           24-MAR-1999;
                                                                                                                                                                                                                                                                              Simmons CR,
                                                                                                       28-SEP-2000
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cggocatgtggttctggatgacggcgcagggaaacaagccgtcgtgccacaacgtcgccc
         tacgccgctggacgccgacggccgccgccgccggcagggtacccggatacggag
                                                   coggogectggacgccgtccgccaccgaccgccgccggaggaggctcccggatatggcc
                                                                    tgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccgg---aacgacgcca
                                                                            aegtegacegeateggetactacacgegetactgeggeatgeteggeaeggecaceggag
                                                                                                                                                                                                                                                                      Promoter; region; rice; chitinase; physical; biological; stress; leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LUMA ITAGMENT CONTG. Chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level expression in roots
                                                                                                                                                                                                                                                                                                                                                     /*tag= _b
/note= "Putative polyadenylation signal"
1093..1098
                                                                                                                                                                                                                                                                                                                                                                    1093..1098
/*tag= c
//note= "putative polyadenylation signal"
                                                                                                                                       gcaacctcgactgctacacccagaggaacttcg 763
                                                                                                                                                         818
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/note= "Region conse...
II chitinases"
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55..1065
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1053..1058
/*tag= b
                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                      RCH10 chitinase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                                                                                                                           Oryza sativa
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                                                                                                                                                                                                                                                                                                                                                      polyA_signal
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The sequence given represents the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this gene in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612
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                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                     Sequence 1151 BP; 197 A; 409 C; 353 G; 192 T; 0 other;
                                                                                                                                                                                                                                                       39.0%; Score 300.6; DB 13; 65.6%; Pred. No. 1.7e-44; iive 0; Mismatches 214;
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                                                                                                                                                                     defence genes and selectable genes.
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                                                                                                                                                                                                                                                                            Similarity
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gtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggaggc 732
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                                                                                                                                                                                                                                        562 gggccggactactgccagcagagcgcgcagtggccgtgccgcgccggcaagaagtactac 621
                                                                                                                               ggcgccgacctgctcggcgacccggacctcgtggcgtctgacgccaccgtctccttcgac 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance transgenic plant; preservation; cryopreservation; tumour; therapy;
                                                                acggccatgtggttctggatgacggcggagggaaacaagccgtcgtgccacaacgtcgcc
                                                                                                                                                                             613 gtgatcaccaatatcatcaacggcggctcgagtgcggaatgggccggaacgacgccaac
                                                                                                                                                                                                                                                                                          553 ctacgccgctggacgccgacggccgccgacaccgctgccggcagggtaccggatacgga
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61..954
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/note= "separately claimed in Claim"
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/note= "separately claimed in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-153795/13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gegggggtgeegegggegeagggegtgggeteggteateaegeggtegtaegegage 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39.0%; Score 300.6; DB 16; Length 1151; llarity 65.6%; Pred. No. 1.7e-44; Conservative 0; Mismatches 214; Indels 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transgenic plants contg. several plant defence associated proteins - have increased resistance to plant pathogens when
                                                                                                               Chitinase; RCH10 gene; transgenic plant; disease resistance; crop improvement; tobacco; Nicotiana tabacum; plant defense; fungus pathogen; Cercospora nicotinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1151 BP; 197 A; 409 C; 353 G; 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 31-32; 45pp; English.
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                                                                                                                                                                                                          Location/Qualifiers
55..1065
/*tag= a
        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   grown in crops as a food source
                                                                                                                                                                                                                                                                                                                                                                                                     Maher EA,
       AAQ81346 standard; cDNA; 1151
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                                                                                                                                                                                                                                                                                                                                               93US-0093372
                                                                                                                                                         Thanatephorus cucumeris; ss
                                                            (first entry)
                                                                                       Rice chitinase RCH10 gene.
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                                                                                                                                                                                    Oryza sativa.
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                                                                                                                                                                                                                                                                                                                                                 16-JUL-1993;
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                                                                                                                                                                                                                                                                                             26-JAN-1995
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                                   AA081346;
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The present sequence encodes winter rye (Secale cerale L. cv. Muskateer) (HT9 preprotein (see AAM98079). Mature CHF9 (see AAM98080) is a chitinase-like protein that has chitinase (antifungal) and antifreeze activities. CHF9 cDNA (ch-9) was obtained by isolating mRNA from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed, and then sorthing the cold-induced chitinase cDNAs to determine which encoded proteins with ice-binding ability. CHF9 and CHF46 (see AAM98081-82) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thallana. The chitinase-like antifreeze proteins can be used: to increase freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               microorganisms exposed to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for cryopreservation and hypothermic protection of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved
                                                 New nucleic acid encoding antifreeze polypeptides from plants particularly with chitinase activity, used to impart frost, and pathogen, resistant to plants, for preservation of foods, cells
                                                                                                                                                                                      Claim 2; Fig 21a; 118pp; English.
P-PSDB; AAW98079, AAW98080.
                                                                                                                                    and for treating tumours
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Sequence 954 BP; 162 A; 335 C; 306 G; 151 T; 0 other;

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                                                                                                         110 acgegageactetgeecaacegegacaactegetgtgeeeggeeagagggttetacaegt 169
                                                                                                                                                                                                                                             436
                                                                                                                                                                                                                                                                                                                             367
                                                                              197 cagtaceggtacegaceceaceggeggeggegtgtectecattatetegeagtegetet 256
                                                                                                                                   257 tegaccagatgetgetgeacegeaacgatgeggegtgeetggeeaaggggttetacaaet 316
                           Gaps
                                                      ---ggacgagaggcgctgccgaccagttccagtggggctactgcttcaaggaagataa
                                                                                                                                                                                                                                                                                                                               --aaggccacgtccccaccat
                                                                                                                                                                                                                                                                                                                                                      ccateggcacggacetactcaacaacccagacetcgtggccacggacgccacgtgtcat
                                                                                                                                                                                                                 230 acgacateaagcgcgacetegccgcettetteggceagaceteceacgagaceacggag
                                                                                                                                                                                                                                  437 ggtggcccacggcgcccgacggcccctactcgtggggctactgcttcaaccaggagcgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                         cgatcgggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtcct
                                                                                                                                                            170 acgaegeetteategeegeegeeaacacetteeegggetteggeaeeaeeggeagegeeg
                                                                                                                                                                                     317 adggogocttoatogoogoogocaactogttotogggottogogacoacgggtggoacog
                                                                                                                                                                                                                                                                                                                                                                                    actatggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagag
                           42;
  Length 954;
                           Indels
  DB 20;
           .9e-44;
nes 221;
            Pred. No. 2.9e
0; Mismatches
 Score 299.4;
Pred. No. 2.9
38.8%;
Local Similarity 65.3%;
hes 494; Conservative
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 Query Match
Best Local S
Matches 494
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The present sequence encodes a chitinase designated RCH10. The specification describes chimcric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomoras spp. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to confer desired traits on essentially any plant.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chimeric plant receptors comprising a polynucleotide encoding a RRK receptor containing a heterologous extracellular domain and a kinase domain from a Xa21 polypeptide, useful for modulating plant responses
tegecetaegeegetggaegeegaeggeegeegaeaeegetgeeggeagggtaeeeggat 607
                                                              299
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                        tgatcacgggccggtggagcccttcgggcgccaggcagcagcgggtagggttgcctgggt
                                                                                                                                                                gtgtcgccgaccgaatcgggttctacaagcgctactgtgacctcctcggcgtcagctacg
                                                                  acggagtgatcaccaatatcatcaacggcggggctcgagtgcggaatgggccggaacgacg
                                                                                                                               668 ccaacgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccg
                                                                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a rice chitinase designated RCH10.
                                                                                                                                                                                                               917 gogacaatctggactgctacaaccagaggccgttcgc 953
                                                                                                                                                                                               gaggeaacetegaetgetaeaeeceagaggaaettege 764
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/product= "chitinase RCH10"
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(SALK ) SALK INST BIOLOGICAL STUDIES.
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                                                                                                                                                                                                                                                                                                              AAF54983 standard; DNA; 3035 BP
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Hordeum vulgare
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                                                                                 mat_peptide
                                                                sig_peptide
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                                                                                                                                                                                                                                 Chet I,
Munây J,
                                                                                                                                                                                                                                                                                                                   vectors
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                                                               gegggggggtgeegegggggggggggggggcteggtcatcacggggtggtggtacgegage 117
                                             Gaps
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                                                                                                                                                                                                                                                                     2446 gggccggactactgccagcagagcgcgcagtggccgtgcgccggccaggaagtactac
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                                                                                                                                                         -cccaccatactat
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                                                                                                                                                                                                                                                                                                                            gggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcagg
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                                                                                                                                      178 ttcatcgccgccaacaccttcccgggcttcggcaccaccggcagcgccgacgtc
                                                                                                                                                                            aagogogacctcgccgccttcttcggccagacctcccacgagaccaccggag---ggacg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antifungal, pathogen; resistance; transgenic organism; synergy; crop protection; transgenic plant; chitinase; glucanase; protein synthesis inhibitor; disease; ss.
                                            45;
                           Length 3035;
                          Score 297.4; DB 22; Length
Pred. No. 5.9e-44;
0; Mismatches 216; Indels
G; 749 T; 0 other;
                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 aacctcgactgctacacccagaggaacttcgct 765
Sequence 3035 BP; 715 A; 832 C; 739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; cDNA; 1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding chitinase G.
                           38.6%;
65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                            Matches 492; Conservative
                          Query Match
Best Local Similarity
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This sequence encodes Chitinase G. Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistant corranisms. The genome of such transgenic organisms preferably contains more then one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so that the transgenic organisms have a greater degree of resistance or resistance against a wider spectrum of diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       geagegigetectecategietegegegeacagitigacegeatgeitetecaecegeaaeg 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transgenic organisms contg. at least 2 pathogen inhibiting genes - esp. plants contg. genes with antifungal activity, show synergistic increase in disease resistance, also new DNA transfer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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/note= "Putative polyadenylation signal."
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Pred. No. 1.3e-43;
0; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
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                                                                                                                                     Ġ
                                                                                                                                     Chitinase
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                                                 Location/Qualifiers
64..864
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Goernhardt B;
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Best Local Similarity 63.8%;
Matches 504; Conservative 0
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                                                                                                        /product= C
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/*tag= c
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part; monocotyledonous plant; bacterial resistance; ds.
cagggoggtccaactacgatcttgccgggagagcgatcgggaaggacctggtgagcaacc
                                                                                                                                   cagacctagtgtccacggacgcggtggtgtccttcaggacggccatgtggttctggatga
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                                                              .---aaggecacgtececaccatactatggacggggacecatecaattga
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/product= "floral-organ specific chitinase"
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                           tecagtggggetactgetteaaggaagagataage
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114..1100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa
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                                                                                                                                  This cDNA encodes a floral organ-specific chitinase. The specification provides a promoter sequence (AAV49083) derived from rice associated with chitinase, specific to floral organs that allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as increased resistance to bacterial attack.
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                             Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of monocotyledonous plants
                                                                                                                                                                                                                                                                                                                                                         Length 1318;
                                                                                                                                                                                                                                                                                                                                                                                          36;
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                                                                                                                                                                                                                                                                                                   Sequence 1318 BP; 231 A; 442 C; 440 G; 205 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     Score 262.2; DB 19;
Pred. No. 8.7e-38;
0; Mismatches 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cagtgggggtactgcttcaaggaagagataagcaag-
                                                                                                    Claim 7; Pages 33-35; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                       34.0%;
62.9%;
                                                                                                                                                                                                                                                                                                                                                                      al Similarity 62.9
490; Conservative
P-PSDB; AAW64776.
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Best Local 3
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  cgccttcttcggccagacctcccacgagaccac---cggagggacgagggggcgctgccga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR-Q cDNA cloned into plasmid pBScht15.
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Moyer MB;
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89US-0329018.
89US-0368672.
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, Neuhaus J-M,
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20-JUN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New maize chitinase genes encoding seven chitinases of glucosyl hydrolase family 19 are useful for enhancing disease resistance in crop plants by modulating its expression in plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 ggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccgcgacaac 138
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1014 ctcggcgtcggctacgggcccaacctggactgcttcggccaggcggcggtcggacggcga 1072
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                                                                                                                                                                                 Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy 18; pathogen control; disease resistance; molecular marker; ss.
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                                                                                                                                                         cDNA encoding a maize chitinase polypeptide designated ZmCh7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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Pred. No. 5.9e-35;
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                                                                                                                                                                                                                                                Location/Qualifiers 32..817
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                                                                              BP.
                                                                              CDNA; 1163
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62.5%;
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Les 466; Conserv
                                                                            AAA96224 standard;
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06-MAR-1989;
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Payne G;
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                                                                                                                                                                                                      131
                                                                                                                                                                                                                          ggcacaaggcattggttctattgtaacgagtgacttgttcaacgagatgctgaagaatag 164
                                                                                                                                                                                   Gaps
                                                   This chimeric DNA sequence comprises the PR-Q plant pathogenesis-
related protein (PRP)-coding sequence,(1), and a promoter sequence
which enhances transcription of (1). This construct is used to
produce transgenic plant cells or -tissues with the ability to re-
generate into plants which are disease resistant.
See also AAQ06179-84, AAQ06186, AAQ06199-Q06208 and AAQ06829.
                                                                                                                                                                                                                                             cgacaactcgctgtgcccggccagagggttctacacgtacgacgccttcatcgccgccgc
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                                                                                                                                                            Length 1010;
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 Disease-resistant transgenic plants - obtd. using encoding a inducible pathogenesis-related protein from infected plants.
                                                                                                                                                                               Indels
                                                                                                                            Sequence 1010 BP; 310 A; 178 C; 239 G; 283 T; 0 other;
                                                                                                                                                           DB 11;
                                                                                                                                                         Score 239.6; DB 11
Pred. No. 7.8e-34;
                                                                                                                                                                               Mismatches
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                               English.
                                                                                                                                                                                0;
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illarity 61.3%;
Conservative
                              77pp;
                               26;
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Best Local Similarity
                              17; page
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RESULT 12
AAN90845
ID AAN90845 standard; cDNA; 1020
AC AAN90845;

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vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence is tobacco PR-Q gene ( PR = pathogenesis-related), cont. in plasmid BESchlīs. PR-Q is a chemically inducible gene used to regulate transcription of an associated DNA sequence in plant tissue. See also AAN90367, AAN90368, AAN90841-N90846, and AAP91383-P91386.
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                                                                      herbicide resistance; pBScht15; transgenic plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 cgacaactcgctgtgcccggccagagggttctacacgtacgacgccttcatcgccgcgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cgggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcag
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                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
                                                                                                                                                                                                                                                                                                                                                                    Meins
                                                                                                                                                                                                                                                                                                                                                                                                                      DNA sequence
to herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1020 BP; 310 A; 182 C; 239 G; 289 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                    Sperisen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemical induction of cloned genes in plants - and processes for inducible expression leading
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                Duesing J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 81; page 79; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                Harms C,
                                                                                                          cv. Xanthi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.1%;
61.3%;
                                                                                                                                                                                                                   89EP-0103888
                                                                                                                                                                                                                                                       88US-0165667
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                            AG.
                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                  Montoya A,
                                                                                                                                                                                                                                                                                                                            WPI; 1989-265342/37
                                                                        Tobacco PR-Q gene;
                                                                                                        Nicotiana tabaccum
                                                                                                                                                                                                                                                                                          GEIGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Chemical induction
                                      gene.
                                    Tobacco PR-Q
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This sequence represents a clone of the tobacco pathogenesis related (PR)

gene. This gene can be isolated using the method of the invention.

The method is for isolating a chemically regulatable DNA promoter

fragment from the 5' flanking region of a chemically regulatable gene in

the controlled expression of genes, under the control of a

consecul for the controlled expression of sequences which will be

consecul for the controlled expression of sequences which will be

connecoding regulatable sequence. This is useful in plants with a

connecoding regulatable sequence. This is useful in plants with a

conficie or pesticide detoxification mechanism under the control of a

conficie or pesticide to give optimal tolerance. The promoter fragment

conficie or pesticide to give optimal tolerance. The promoter fragment

controlling sequences which encode traits such as

controlling sequences which encode traits such as

controlling to dishappenent, make or female sterility, and the ability

cof the plant to withstand cold, heat, salt and drought. The chemical

induction of the promoter allows the regulation of production of

compounds, e.g. flavours, fragrances, pigments, natural sweeteners,

industrial feedstocks, antimicrobials and pharmaceuticals, by

compounds, e.g. flavours, interprobals and pharmaceuticals, by

biosynthesis or metabolite conversion, whose blosynthesis is controlled

by endogenous or foreign genes. The method allows control over the time

cand rate of gene expression either throughout the whole plant, or in

concalized tissues, to achieve e.g. fungal or insect resistance by for

instance dusting the leaves with the chemical regulator. Controlling the
    611
                                                                                                       696 ggaagatcgaattggatactacaggaggtattgtggtatgttaaatgttgctccgggggga 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pesticide;
                                                                                     agtgatcaccaatatcatcaacggcgggctcgagtgcggaatggggccggaacgacgcaa
    cetacyccyctygyacyccyacygccyacyccyacaccyctyccygycayyytacccygatacyy
                                                                                                                                                                         cytcyaccycatcygctactacacycyctactycygcatyctcygcacygccaccygagg
                                          categgtegttggaeteegtetgeegeggateaggeggegaategagtaeeaggttaegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolating chemically regulatable DNA sequences in plants - useful for chemically controlling expression in transformed plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chemically regulatable DNA promoter; expression control; herbicide tolerance; pathogenesis related gene; PR gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 46; Column 177-180; 175pp; English.
                                                                                                                                                                                                                                                        763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tobacco PR-Q gene clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nicotiana acuminata
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developmental processes by the application of a regulating chemical in e.g. the commercial production of cultivated crops allows processes such as germination, flower formation and fruit ripening to be synchronised at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311
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                                                                                                                                                                                                                                                                                                                                                                                                                               312 gttccagtggggctactgcttcaaggaagagataagcaaggccacgtccccaccatacta 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tggacggggacccatccaattgacagggcggtccaactacgatctgccgggagagcgat 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 tggtagaggacccatccaattgacaaaccgaaataactatgagaaagctggaactgcaat 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 456 tggacaagagctagttaacaaccctgatttagtggccacagatgctactatatcattcaa 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  672 cgtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggagg 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        696 ggaagatcgaattggatactacaggaggtattgtgggtatgttaaatgttgctccggggga 755
                                                                                                                                                                                                                                                                                 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gaeggeeatgtggttetggatgaeggegeagggaaacaageegtegtgeeacaaegtege 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulation; transcription; plant tissue; chimeric construction; PR; pathogenesis-related protein; anti-pathogenic; transgenic plant;
                                                                                                                                                                                                                                                                                 105 ggcacaaggcattggttctattgtaacgagtgacttgttcaacgagatgctgaagaatag
                                                                                                                                                                                                                                                                                                                                                              165 gaacgacggtagatgtcctgccaatggcttctacacttatgatgcattcatagctgctgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 tgcctttttcggtcaaacttctcacgaaactactggtggatccctgagtgcag--aacca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            576 categgiegitegiactecgietgeegeggateaggeggegaategagtaeeaggitaegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            636 tgtaattaccaacatcattaacggtggaattgaatgtggcataggacggaatgacgcagt
                                                                                                                                                                                                                                           72 ggcgcagggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        552 cetacgecgetggacgecgaeggecgecgecgecgetgeeggeagggtaeeeggataegg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 cgccttcttcggccagacctcccacgagaccacggaggacgaggagggcgctgccgacca
                                                                                                                                                                                                                                                                                                                                                                                                        caacaccttcccgggcttcggcaccaccggcagcgacgacgacatcaagcgcgacctcgc
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                                                                                                                                                               DB 20; Length 1020;
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                                                                                                  Sequence 1020 BP; 310 A; 181 C; 240 G; 289 T; 0 other
                                                                                                                                                         Score 239.6; DB 20;
Pred. No. 7.8e-34;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PR-Q protein encoding cDNA sequence.
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                                                                                                                                                             31.1%;
61.3%;
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                                                                                                                                                         Query Match 31.1'
Best Local Similarity 61.3'
Matches 424; Conservative
                                                               a given time.
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ID AAV7
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Sela-Buurlage MB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a DNA molecule encoding a pathogenesis-related (PR) protein having beta-1,3-glucanase activity selected from PR-2, PR-2', PR-N', PR-N PR-0 and PR-0'. Also described are: (i) a chimeric gene comprising the above DNA molecule linked to a heterologous promoter; (ii) a vector containing the chimeric gene; (iii) a best cell containing the chimeric gene; (iv) a transgenic plant. The DNA molecule is used to produce transgenic plants are book molecule is used to produce transgenic plants disease or pest resistance. The present sequence represents a tobacco PR-Q protein encoding cDNA sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding pathogenesis-related glucanase proteins - useful for producing transgenic plants with enhanced disease or pest resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cgccttcttcggccagacctcccacgagaccaccggagggacgagggggcgctgccgacca
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ن
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beta-1,3-glucanase activity; pest resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 239.6; DB 20;
Pred. No. 7.8e-34;
); Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                            Example 46; Column 171-174; 169pp; English.
                                                                                                                                                                                                                                                                                                                                               Ward ER;
                                                                                                                                                                                                                                                                                                                                               Ryals JA,
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0
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900S-0580431.
900S-0632441.
910S-0678378.
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ilarity 61.3%;
Conservative (
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BBUS-0165667.
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                                                                                                                  31-MAY-1995;
08-MAR-1988;
06-FEB-1989;
                                                                                                                                                                                                                                                                                   16~JUL-1993;
13-JAN-1994;
                                                                                                                                                                                                                                   06-MAR-1992;
06-NOV-1992;
06-APR-1993;
                      Nicotiana sp
                                                                                             31-MAY-1995;
                                                                                                                                                      24-MAR-1989;
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21-DEC-1990;
                                                                                                                                                                                                                          27-SEP-1991;
                                             US5847258-A.
                                                                                                                                                                   JUN-1989;
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                                                                                                                                                                                                                                                                          12-APR-1993;
                                                                   08-DEC-1998
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                                                     tggtagaggacccatccaattgacaaaccgaaataactatgagaaagctggaactgcaat
                                                                                                       456 tggacaagagctagttaacaaceetgatttagtggccacagatgctactatatcattcaa
                          tggacgggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgat
                                                                                                                                   gacggccatgtggttctggatgacggcgcaggggaaacaagccgtcgtgccacaacgtcgc
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Woloshuk CP,
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, Vloemans AA,
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Example 4; Fig 1; 55pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 671
                                                                                                                                                                                                              Gaps
                                This sequence was isolated from a P.hybrida cDNA library. It has 80 per cent homology with tobacco clone PROB30 which encodes extracellular chitinase PR-Protein R. The gene can be inserted into an appropriate plasmid for production of transgenic plants having resistance to fungal pathogens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             507 aacagcaatatggttctggatgacaccacagggtaacaagccatcttgccacgacgttat
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                                                                                                                                                                                                              3;
                                                                                                                                                                                 Length 965;
                                                                                                                                                                                                              Indels
                                                                                                                                      Sequence 965 BP; 300 A; 173 C; 218 G; 274 T; 0 other;
                                                                                                                                                                              Query Match 30.5%; Score 235.4; DB 12; Best Local Similarity 59.7%; Pred. No. 4.2e-33; Matches 414; Conservative 0; Mismatches 276;
                                                                                                                                                                                DB 12;
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completed: May 3, 2002, 16:32:02 ne: 6956 sec

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CITY: Los Angeles
STATE: Callfornia
connTRY: United States
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TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
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Best Local Similarity
Matches 494; Conserv
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LOCATION:
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1225.795 Million cell updates/sec
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                                                                                                                                                                                                                                                                                       771
1 atggcgaggtttgctgccct.....agaggaacttcgctagctag 771
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Sequence 9,
Sequence 7,
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                                                                                                                                                  3, 2002, 14:25:26 ; Search time 142.45 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-456-740-7
US-08-456-240-7
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US-08-97-1217-7
US-08-97-1217-7
US-08-047-413-8
US-08-1217-7
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US-08-138-873A-9
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US-08-144-803-7
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US-08-449-043-7
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US-08-455-416-7
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Maximum Match 100%
Listing first 45 summaries
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Patent No. 5399680
GENERAL INFORMATION:
GENERAL LINFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: LAMB PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: PETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGANT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 300.6; DB 1;
Pred. No. 1.1e-51;
0; Mismatches 214;
       US-08-475-427-15
US-07-842-165-15
US-08-047-413-10
US-08-229-050-10
                                                                                                                                                                                                                  ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P31 8899 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Lamb, Christopher J.
APPLICANT: Zhu, Qun
APPLICANT: Maher, Eileen A.
APPLICANT: DAVON Richard A.
TITLE OF INVENTION: TRANSCENIC PLANTS CONTAINING MULTIPLE
TITLE OF INVENTION: DISEASE RESISTANCE GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
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Patent No. 5530187
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CITY: Los Angeles
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ZIP: 90071-2921
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US-08-093-372-1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: STREM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 300.6; DB 1;
Pred. No. 1.1e-51;
0; Mismatches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: /product= "RICE CHITINASE"
US-08-093-372-1
                                                                                       .....: US/08/093,372
16-JUL-1993
7N: 800
                                                                                                                                                CLASSIFICATION.
ATTORNEY/AGENT INFORMATION.
NAME: Reler's Chephen B.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 935
TELECHMONE: 619-546-437
TELEPHONE: 619-546-9392
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39.0%;
65.6%;
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Best Local Similarity 65.6
Matches 494; Conservative
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LOCATION: 55..1062
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118 actetgeceaacegegacaactegetgtgeceggecagagggttetacaegtacgaegec 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New YORK
COUNTRY: U.S.A.
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                      613 gtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgacaac
                                                  862 GTCATCACCAACATCATCAACGGCGGGCTGGAGTGCGGCCATGGCGAGGACGATCGCATC
                                                                                   gtcgaccgcatcggctactacacgcgctactgcggcatgctcggcacggccaccggaggc
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APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE REGULATORY
TITLE OF INVENTION: BLEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCES: 26
ADDRESSES: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMUTER: IBM FO COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/379,259
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.0%; Score 300.6; DB 1;
65.6%; Pred. No. 1.1e-51;
iive 0; Mismatches 214;
                                                                                                                                                                              982 AACTIGGATIGCTACAGCCAGAGGCCTICGGCT 1014
                                                                                                                                                 aacctcgactgctacacccagaggaacttcgct 765
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REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEPAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                         Sequence 2, Application US/08379259
Patent No. 5695939
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1151 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Los Angeles
California
Y: United States
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Matches 494; Conservative
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; LOCATION:
US-08-379-259-2
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                                                                                                                                                                                                                                                                                                                                                                                                       562 GGGCCGGACTACTGCCAGCAGAGCGCGCAGTGGCCGTGCGCCGCCGGCAAGAAGTACTAC 621
                                                                                                                                                                                                                                                  322 ATGCTGCTCCACCGCAACGATGCGGCGTGCCCGGCCAGCAACTTCTACACCTACGACGCC
                                                  ttcatcgccgccgacacacttcccgggcttcggcaccaccggcagcgccgacgacatc
                                                                                                                                                       aagogcgacctcgccgccttcttcggccagacctcccacgagaccaccggagg---ggacg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08457797A
Patent No. 5689045
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic pathogen-resistant organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza CITY: New York
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Sequence 9, Application US/08612025
Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
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US-08-812-025-9
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesil and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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LOCATION: 905..910
OCHER INFORMATION: //note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRATURE:
NAME/KEY: sig_peptide
LOCATION: 296.312.
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 862..1002
OCHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 295.6; DB 1; 63.8%; Pred. No. 1e-50; Live 0; Mismatches 244;
                          REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEFAX: (212) 765-2519
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 64..294
OTHER INFORMATION: /note= "p
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 349...378
OTHER INFORMATION: /note= "p
OTHER INFORMATION: sequence"
18,839
                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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LOCATION: 349..378
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; LOCATION: 133..861
US-08-457-797A-9
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LOCATION: 466..588
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LOCATION: 607..861
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REGISTRATION NUMBER: REGISTRATION NUMBER:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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Matches 504; Conserv
                                                                                                                                                                                                                                                                                NAME/KEY: 5'UTR
LOCATION: 1..63
                                                                                                                                                                                                                                                                                                                              NAME/KEY: CDS
LOCATION: 64.
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CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
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OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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US-09-138-873A-9
; Sequence 9, Application US/09138873A
; Patent No. 6271438
                                                                                                                                   38.38;
63.88;
                                                                                                                                 Query Match 38.39
Best Local Similarity 63.89
Matches 504; Conservative
                                                 mat_peptide
133..861
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851 GACCCTTCGC 860
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                                                 ; NAME/KEY:
; LOCATION:
US-08-812-025-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        257
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/function= "chitinase"
/function= "26 KD preprotein of chitinase G (ChiG)"
/product="11fungal activity, especially on Trichoderma reesii and Fusarium sporotrichoides as well as Rhizoctonia solani and Botrytis cinerea."
              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Fatentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: polyA_signal
LOCATION: 95.910
OCHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---- LAKURMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "probable signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 862...1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
                                                                                                                                                                             NAME: KOLE, Lisa
REGISTRATION NUMBER: 35,225
REFORMUNICATION NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEPHONE: (212) 765-2519
TELERA: 23855
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 349.378

COCHER INFORMATION: /note= "probable signal OTHER INFORMATION: sequence"
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OTHER INFORMATION: /note= "probable signal
OTHER INFORMATION: sequence"
                                                                                                                                                 NAME: Tenser, Arthur REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Hordeum vulgare STRAIN: L.
                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Tenser, Arthur
                                                                                                                                                                                                                                                                                                                                      LENGIH: 1002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /no
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607..861
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LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: sec
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                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: single
   COMPUTER READABLE FORM:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..63
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                                                                                                                   FILING DATE:
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LOCATION:
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71 GGTTGGGGGTGGTGGTGGTAGCCACGGTGGCCATGGCCATCGGCACGGCGCGCG 130
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                                                                                                                                                                                                                                  131 GCAGCGTGTCCTCCATCGTCTCGGGGGCACAGTTTGACCGCATGCTTCTCCCACGCAAC3 190
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                                                 42;
  Length 1002;
                                                 Indels
Score 295.6; DB 1;
Pred. No. 1e-50;
0; Mismatches 244;
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NAME/KEY:
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US-09-138-873A-9
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reseli and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                        Transgenic pathogen-resistant organism
                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
COMPUTER: IBM FC compatible
OFBRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION DATE: ALOYOS/138, 873A
FILING DATE: AUGUST 24, 1998
ATTOREX/AGENT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
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LOCATION: 905..910
OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFBRENCE/DOCKET NUMBER: A295
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEPAX: (212) 765-2519
TELEPAX: 238655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                           SEE: Baker & Botts
: 30 Rockefeller Plaza
New York
                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1002 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: sig_peptide
LOCATION: 64..294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /nc
OTHER INFORMATION: see
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                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
                                      TITLE OF INVENTION:
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LOCATION: 1..63
                                                                                                                                               STATE: New York COUNTRY: U.S.A. ZIP: 10112
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GENERAL INFORMATION:
APPLICANT:
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                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77 agggcgtgggctcggtcatcacgcggttcggtgtacgcgagcactctgcccaaccgcgaca 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               131 geagegratecrecaregreregegeacagriticacegeargerrerecacegeaace 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 ACGGCGCCTGCCAGGCCTTCTACACCTACGACGCCTTCGTCGCCGCCGCCGCAGCGG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --aaggccacgtccccaccatactatggacggggacccatccaattga 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 1002;
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                                                                                                                                                                                                             LOCATION: 607. 861
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                        /note= "probable signal peptide
                                                                                                                    /note= "probable signal peptide
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                    Score 295.6; DB 4;
Pred. No. 1e-50;
0; Mismatches 244;
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LOCATION: 349..378
COTHER INFORMATION: Sequence"
COTHER INFORMATION: Sequence"
FEAUTR:
NAME/KEY: sig_peptide
LOCATION: 466..588
COTHER INFORMATION: Anote= "pro
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Best Local Similarity 63.8%;
Matches 504; Conservative
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133..861
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312 gitccagiggggctacigcitcaaggaagaataagcaaggccacgiccccaccaiacia 371
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Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                  S-19825/P1/CGC 1727
                                                                                FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATE: 20-UN-1989
PRIOR APPLICATION DATE: 24-MAR-1989
PRIOR APPLICATION DATE: 24-MAR-1989
PRIOR APPLICATION DATE: 24-MAR-1993
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 36,129
REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/COCKET NUMBER: 5-19825/P1,
TELECHONE: (919)541-8614
ITELEPHONE: (919)541-8614
ITELEPHONE: (919)541-8619
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
TOWNSHIP TOWNSHIPSITESISTICS:
                                                  US 07/768,122
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Best Local Similarity 61.3%;
Matches 424; Conservative
                                                                          27-SEP-1991
                   FILING DATE: 6-MAR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
FILING DATE: 27-SEP-
APPLICATION NUMBER:
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  791 AGCGCTACTGTGACATCCTCGGCGTTGGCTACGGCAACAACCTCGATTGCTACAGCCAGA 850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/181,271A
FILING DATE: 13-JAN-94
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APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
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APPLICATION UNDBER: US 07/305,566 FILING DATE: 6-FEB-1989
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Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Patent No. 5614395
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Sperison, Christoph
Stinson, Jeffrey R.
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Alexander, Danny C.
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Neuhaus, Jean-Marc
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PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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FILING DATE: 21-DEC
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STATE: New York
                                                755 ggaacttcgc 764
                                                                                       851 GACCCTTCGC 860
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APPLICANT: RVALS
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APPLICANT:
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                             636 TGTAATTACCAACATCATTAACGGTGGAATTGAATGTGGCATAGGACGGAATGACGCAGT 695
612 agtgatcaccaatatcatcaacggcgggtcgagtgcggaatgggccggaacgccaa
                                                                                           672 egtegacegeateggetactacacegegetactgeggeatgeteggeacggecaceggagg
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC FITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF NUMBER OF SEQUENCES: 106
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,315
FILING DATE: 24-MAY.1995
CLASSIFICATION: 800
                                                                                                                                        732 caacctcgactgctacacccagaggaacttcg 763
                                                                                                                                                                         756 AAACTTGGACTGTTACAACCAAAGGAACTTCG 787
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APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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Montoya, Allice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
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APPLICATION NUMBER: 08/181,271
PIT.ING DATE: 13-JAN-94
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Alexander, Danny C.
Beck, James J.
Puesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
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Patent No. 5650505
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                    Harms, Christian
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MEDIUM TYPE: Floppy
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US-08-449-315-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGATGCTGAAGAATAG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         225 CAATTCCTTTCCTGGTTTTGGAACTACTGGTGATGATACTGCCCGTAGGAAAGTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
31.1%; Score 239.6; DB 1;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S-19825/P1/CGC 1727
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US C7/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION NUMBER: US 07/329,018
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1983
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                 PELLING DATE: 20-0CT 1989
PRIOR PAPLICATION NUMBER: US 07/425,504
PRIOR PAPLICATION DATA: APPLICATION NUMBER: US 07/848,506
PRIOR DATE: 6-WAR-1992
RAPPLICATION PAPR: APPLICATION DATE: TILING DATE: 27-5EP-1991
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                PALLING CATALON DATA:
PRIOR PAPLICATION NUMBER: US 07/580,431
FTIING DATE: 7-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott
REGISTRATION UNDRER: 36,129
REPERBUCK/DOCKET NUMBER: 5-19
RELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8614
TELEPAX: (919) 541-8619
INFORMATION FOR SEQ. ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1020 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-449-315-7
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BER: US 07/678,378
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8614
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61.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEÓ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1020 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (919)541-8689
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Best Local Similarity 61.3
Matches 424; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
EDNESS: single
   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                    696 GGAAGATCGAATTGGATACTACAGGAGGTATTGTGGTATGTTAAATGTTGCTCCGGGGGA 755
       456 TGGACAAGAGCTAGTTAACAACCCTGATTTAGTGGCCACAGATGCTACTATATCATTCAA 515
                                        gacggccatgtggttctggatgacggcgcagggaaacaagccgtcgtgccacaacgtcgc 551
                                                                                                                                     CATCGGTGGTTGGACTCCGTCTGCCGCGGATCAGGCGGCGAATCGAGTACCAGGTTACGG
                                                                                                                                                                                   612 agtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgacgcaa
                                                                         516 AACAGCTATATGGTTTTGGATGACACCACAGGACAACAAGCCATCTTCCCACGACGTTAT
                                                                                                             cctacyccyctyyacyccyacyccyccyacaccyctyccyycayyytacccyyatacyy
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,803
FILING DATE: 19-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                        caacetegaetgetacaeceagaggaaetteg 763
                                                                                                                                                                                                                                                                                                                                           LU6
LADRESS:
AUDRESS:
CLBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: New York
COUNTRY: US^A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ryals, John A.
Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
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Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/08444803
Patent No. 5654414
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Moyer, Mary B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08, FILING DATE: 13-JAN-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 13-JAN-9
APPLICATION NUMBER: C
FILING DATE: 16-JUL-1
PRIOR APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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CLASSIFICATION:
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APPLICANT:
APPLICANT:
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APPLICANT:
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285 IGCCITTICGGICAAACTICICAGGAAACTACIGGIGGATCCCIGAGIGCAG--AACCA 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caacacetteeegggetteggeaceaceggeagegeegaegacateaagegegeetege 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 ggcgcagggcgtgggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaaccg 131
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Pred. No. 1.3e-39;
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0; Mismatches 259;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION PARE:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY AGENT INFORMATION:
PRIOR APPLICATION NOMES:
PRIOR APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
APPLICATION NATA:
PRIOR APPLICATION NATA:
PRIOR APPLICATION NATA:
APPLICATION NAMER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NAMER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION NAMER: US 07/632,441
FILING DATE: 20-0CT 1989
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAY-1992
PRIOR APPLICATION DATA:
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                               FILING DATE: 13-JAN-94
APPLICATION WUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION WUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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24-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/045,957 FILING DATE: 12-APR-1993 ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
FILING APPLICATION DATA.

APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
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                                                                                                                                                                    BER: US 07/678,378
-APR-1991
                                                                                                                                                                                                                                                                                                                                            UMBER: US 08/042,847
6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                         JMBER: US 07/632,441
21-DEC-1990
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20-OCT 1989
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              08/181,271
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REFERENCE/DOCKET UNDBER: S-1
TELECOMMUNICATION: TREEDHONF:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Elmer, James Scott REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0'
FILING DATE: 27-SEP-1991
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APPLICATION NUMBER: US
FILING DATE: 21-DEC-19
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: US
FILING DATE: 20-OCT 19
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EDNESS: single
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 6-APR-19
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                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
FILING DATE: 7-SEP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; MOLECULE TYPE: CDNA US-08-449-043-7
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                                                                                                                                     491
                                                                                                                                                                                                                                                       516 AACAGCTATATGGTTTTGGATGACCACCAGGACAACAAGCCATCTTCCCACGACGTTAT 575
                                                          tggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagagcgat 431
                                                                                                                                                                                                                                                                                                                                                                                                         612 agtgatcaccaatatcatcaacggcgggctcgagtgcggaatgggccggaacgacgccaa
                                                                                                                                                                                                                    492 gacggccatgtggttctggatgacggcgagggaaacaagccgtcgtgccacaacgtcgc
                                                                                   ----AGATATIA
                                                                                                                                       432 cgggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcag
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343 TITACAGGAGGGTATTGCTTTGTTAGGCAAAATGACCAGAGTGAC
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/08/449,043
FILING DATE: 24 MAY-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732 caacetegactgetacacecagaggaactteg 763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Meins, Jr., Frederick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08449043
Patent No. 5689044
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Goodman, Robert M.
Harms, Christian
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Sperison, Christoph
Stinson, Jeffrey R.
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Beck, James J.
Duesing, John H.
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Moyer, Mary B.
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APPLICANT:
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APPLICANT:
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US-08-449-043-7
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STATE:
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132 cgacaactogctgtgcccggccagaggttctacacgtacgacgccttcatcgccgccgc 191
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Pred. No. 1.3e-39;
0; Mismatches 259;
ELLING DATE: 16-JUL 1993
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 07/937 107
FILING DATE: 6-NOW-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 27-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-UN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
FILING DATE: 24-MAR-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     PHILDR APPLICATION DATA:

APPLICATION NUMBER: US 07/578,378
FILING DATE: 1-APPL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
RILING DATE: 8-YAR-1988
PRIOR APPLICATION NUMBER: US 08/042,847
RILING DATE: 6-APR-1993
RILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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27-SEP-1991
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REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (919)541-8587
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Best Local Similarity 61.3%;
Matches 424; Conservative (
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INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                    372 tggacggggacccattccaattgacagggcggtccaactacgatcttgccgggagagagcgat 431
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                                                                                                                                456 TEGACAAGAGCTAGTTAACAACCCTGATTTAGTGGCCACAGATGCTACTATATCATTCAA
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                                       caacacetteeegggetteggeaceaeeggeaggegeegaegaeateaagggegaeetege
                                                                                 343 TITACAGGAGGGTATIGCTITGTTAGGCAAAATGACCAGAGTGAC-----AGATATIA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/456,265A
FILING DATE: 31-WAY-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: CIBA-GEIGY Corporation
STREET: 520 White Plains Road, P.O. Box 2005
STREET: Tarrytown
STATE: New York
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APPLICANT: Alexander, Danny C.
APPLICANT: Ryals, John A.
APPLICANT: Ryals, John A.
APPLICANT: Stinson, Jeffrey R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE ANI
TITLE OF INVENTION: DNA SEQUENCES AND USES THE
NUMBER OF SEQUENCES: 111
CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: US 08/181,271
FILING DATE: 13-JAN-1994
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OFERATING SYSTEM: PC-DOS/MS-DOS
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636 TGTAATTACCAACATCATTAACGGTGGAATTGAATGTGGCATAGGACGGAATGACGCAGT 695
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252 egeettetteggeeagaeeteeeaegagaeeaeeggaggagggaegagggggegetgeegaeea 311
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                                                                                         gttecagtggggetactgettcaaggaagagataagcaaggecacgtececaccatacta
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TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beck, James J.

Buesing, John H.

Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
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Williams, Shericca C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neuhaus, Jean-Marc
Payne, George B.
Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SULT 12
5.08-455-416-7
Sequence 7, Application US/08455416
Patent No. 5777200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alexander, Danny C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Uknes, Scott J.
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STREET: / on.
TTY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Ryals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New York
: USA
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APPLICANT:
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SUFERNT APPLICATION Release #1.0, Version #1.25
ADPLICATION DATA:
FILING DATE: 31-MAY-1995
GLASSIFICATION: 800
NICH APPLICATION: 800
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Pred. No. 1.3e~39;
0; Mismatches 259;
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ON DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1903
                                                                                                                                                                                                                                                                                                                    PRIOR DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/169 6677
FILLING DATE:
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APPLICATION NUMBER: US 07/632,441
FITTING DATE: 21-DEC-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 20-OCT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-5EP-1990
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24-MAR-1989
                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 07/368,672
                                                                                                                                                                       US 08/093,301
                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 36,129
REFERENCE/DOCKET NUMBER: S-1
TELECOMMONICATION INFORMATION:
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61.38;
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                                                                                                                                                                                        16-JUL-1993
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 61.3
Matches 424; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 20-JUN-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 24-MAR-19
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
PRIOR APPLICATION NUMBER: US
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EDNESS: single
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APPLICATION NUMBER: C
FILING DATE: 27-SEP-1
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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TOPOLOGY: li
                                                                                                                                                                                            FILING DATE:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/368,672
FILING DATE: 20-JUN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/329,018
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APPLICATION NUMBER: US 07/580,431
FILING DATE: 7-SEP-1990
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24-MAR-1989
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APPLICATION NUMBER: US 08/045,957
FILING DATE: 12-APR-1993
ATTORNEY/AGENT INFORMATION:
ADDRESSEE: CIBA-GEIGY Corporation
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INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Elmer, James Scott
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (919)541-8614
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STRANDEDNESS: single
      STREET: 7 SAZ--CITY: Hawthorne
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                                  CITY: Hav
STATE: NE
COUNTRY:
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                                                                                                                                                                                                                 gttccagtggggctactgcttcaaggaagagataagcaaggccacgtccccaccatacta 371
                                                                                                                                                                                                                                                                                                                                                                                                                              432 egggaaggacetggtgagcaacccagacetagtgtecacggacgcggtggtgtecttcag 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516 AACAGCTATATGGTTTTGGATGACCACCACAACAACAAGCCATCTTCCCACGACGTTAT 575
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                                                                                                                                                                                                                                                                                                              343 TITACAGGAGGGTATTGCTTTGTTAGGCAAATGACCAGAGTGAC-----AGATATTA 395
                                                                                                                                                                                                                                                                                                                                                     tggacggggacccatccaattgacagggcggtccaactacgatcttgccgggagggggt 431
                                        132 cgacaactcgctgtgcccggccagaggttctacacgtacgacgccttcatcgccgccgc 191
                                                                             224
105 GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGATGCTGAAGAATAG 164
                                                                                                                   caacacetteecegggetteggeaceaceggeageggeggegaegteaagegegaeetege
                                                                                                                                            cyccttcttcggccagacctcccacgagaccacgagaggacgagaggcgctgccgacca
                                                            APPLICANT: Uknes, Scott J.
APPLICANT: Ward, Eric R.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        732 caacctcgactgctacacccagaggaacttcg 763
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Alexander, Danny C.
Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
Sperison, Office B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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APPLICANT:
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APPLICANT:
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US-08-455-244-7
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APPLICANT:
APPLICANT:
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APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                           CUCKELL AFFLLCATION NUMBER: US/08/455,244
FILING DATE: 31-MAX-1995
CLASSIFCATION: 435
FRICA PELICATION SATA:
APPLICATION NUMBER: 08/181,271
FILING DATE: 13-JNN-94
APPLICATION NUMBER: 08 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 16-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 1-APP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 0-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 0-MAR-1988
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PILING DATE: 20-0CT 1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION PARE:
APPLICATION NUMBER: US 07/768,122
FILING DATE: 27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,441
FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
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TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
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REFERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRILIGATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-7AN-94
APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-UUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
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20-JUN-1989
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                                                                                                                                                                                                 CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                       Uknes, Scott J.
Ward, Eric R.
Williams, Shericca C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08/181,271
Sperison, Christoph
Stinson, Jeffrey R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7-SEP-1990
                                                                                                                                                                                                                    : 7 Skyline Drive
Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 27-SEP-19
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US
FILING DATE: 7-SEP-199
                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                   NUMBER OF SEQUENCES: 1(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 12-AP
                                                                                                                                                                                                                                                               New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                               STATE:
                                                                                                            3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 TGCCTTTTTCGGTCAAACTTCTCACGAAACTACTGGTGGATCCCTGAGTGCAG--AACCA 342
                                                                                                                                                                                                                                                                                                                                                                                                                       311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 TGGTAGAGGACCCATCCAATTGACAAACCGAAATAACTATGAGAAAGCTGGAACTGCAAT 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       egggaaggacctggtgagcaacccagacctagtgtccacggacgcggtggtgtccttcag 491
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                                                                                                                                                        ggegeagggegtgggeteggteateaegeggteggtgtaegegageaetetgeeeaaeeg 131
                                                                                                                                                                                                                                           105 GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGATGCTGAAGAATAG 164
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 CATCGGTCGTTGGACTCCGGCTCTGCCGCGGATCAGCCGAATCGAGTACCAGGTTACGG
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                                                                                                                                                                                                                                                                                                                                    caacacetteccogggetteggcaccaccggcagegecgacgacatcaagegegecetege
                                                                                                                                                                                                                                                                                                                                                                            252 cgccttcttcggccagacctcccacgagaccaccggagggacgaggggggcgctgccgacca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    343 ITTACAGGAGGGTATTGCTTTGTTAGGCAAAATGACCAGAGTGAC-----AGATATTA
                                                                                                            6
                                                                Length 1020;
                                                                                                            Indels
                                                                Score 239.6; DB 1;
Pred. No. 1.3e-39;
0; Mismatches 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    732 caacctcgactgctacacccagaggaacttcg 763
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Montoya, Alice
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Beck, James J.
Duesing, John H.
Friedrich, Leslie B.
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Patent No. 5804693
GENERAL INFORMATION:
APPLICANT: RYALS, John A.
APPLICANT: Beck, James J.
APPLICANT: Beck, James J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moyer, Mary B.
Neuhaus, Jean-Marc
Payne, George B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goodman, Robert M.
Harms, Christian
                                                              31.1%;
ilarity 61.3%;
Conservative
                                                                Query Match
Best Local Similarity
Matches 424; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
APPLICANT:
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APPLICANT:
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US-08-454-876-7
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    US-08-455-244-7
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APPLICANT: Ward, Eric R.
APPLICANT: Williams, Shericca C.
TITLE OF INVENTION: CHEMICALLY REGULATABLE AND ANTI-PATHOGENIC
TITLE OF INVENTION: DNA SEQUENCES AND USES THEREOF
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUFFWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,364
FILING DATE: 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/678,378
FILING DATE: 1-APR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/305,566
FILING DATE: 6-FEB-1989
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6-FEB-1989
N пат.
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APPLICATION NUMBER: US 07/165,667
FILING DATE: 8-MAR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/042,847
FILING DATE: 6-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 21-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/425,504
FILING DATE: 20-OCT 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/848,506
FILING DATE: 6-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/768,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/580,431 FILING DATE: 7-SEP-1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/093,301
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/937,197
FILING DATE: 6-NOV-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/632,441 FILING DATE: 21-DEC-1990
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27-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                CIBA-GEIGY Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
               Friedrich, Leslie B.
Goodman, Robert M.
Harms, Christian
Meins, Jr., Frederick
Montoya, Alice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/181,271
FILLING DATE: 13-JAN-94
APPLICATION NUMBER: US 08/093,
                                                                                                                                                                                       Sperison, Christoph
Stinson, Jeffrey R.
                                                                                                                          Moyer, Mary B.
Neuhaus, Jean-Marc
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FILING DATE: 20-JUN-1989
                                                                                                                                                                     Payne, George B.
John H.
                                                                                                                                                                                                                                 Uknes, Scott J.
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: CIBA-GEIGY Co
STREET: 7 Skyline Drive
CITY: Hawthorne
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: New York COUNTRY: USA
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APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                     GGCACAAGGCATTGGTTCTATTGTAACGAGTGACTTGTTCAACGAGAGGAGTAG 164
                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                    259;
                                                                                                                                                                                                                                                          Score 239.6; DB 1
Pred. No. 1.3e-39;
0; Mismatches 259
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Patent No. 5847258
GENERAL INFORMATION:
APPLICANT: Ryals, John A.
APPLICANT: Beck, James J.
                                                                                ; TYPE: nucleic acid
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-454-876-7
                                                                                                                                                                                                                                                            11.1%;
al Similarity 61.3%;
424; Conservative
    TELEPHONE: (919)541-8614
TELEBRAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 424; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-457-364-7
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31.1%; Score 239.6; DB 2; Length 1020;
Best Local Similarity 61.3%; Pred. No. 1.3e-39;
Matches 424; Conservative 0; Mismatches 259; Indels 9;
FILING DATE: 24-MAR-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/045,957

FILING DATE: 12-APR-1993

ATTORNEY/AGENT INFORMATION:

NAME: Elmer, James Soult

REGISTRATION NUMBER: 36,129

REFERENCE/DOCKET NUMBER: 36,129

REPERENCE/DOCKET NUMBER: S-19825/P1/CGC 1727

TELEPHONE: (919)541-8614

TELEPHONE: (919)541-8614

TELEPHONE: (919)541-8689

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1020 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA
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756 AAACTIGGACTGITACAACCAAAGGAACTICG 787

Search completed: May 3, 2002, 16:26:33 Job time: 7267 sec

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HV_CED001 WHE0667_G HV_CEa001 HVSMEa001

HV_CED000 WWS05.GBR HVSMEf001

WHE0505_G

HVSMEa000

HVSMEa000 WHE0562_G Zm10_06h0 Talr1156A HV_CEa000

19 HV_CEa001 C72797 Rice

HVSME1000

707097F10 HVSMEh010

DB DB

Minimum Maximum

Searched:

Sequence:

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Database

No.

Sc02_08b0 HVSMED001

HVSMEh009 HVSME1000 945005H06

Zm10_02h0 945020E07

Zm10_03a0

HVSMEK000

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on:

Run

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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
; Triticeae; Hordeum.
; Triticeae; Hordeum.
; Wing, R., Glose, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BF065825 906 bp mRNA EST 09-MAR-2001
HV_CEb0014B14f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEb0014B14f, mRNA sequence.
BF065825. GI:13265390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development of a genetically and physically anchored EST resource for barley genomics (pubblished (2000) 0n Oct 17, 2000 this sequence version replaced gi:10842464.
                                                       BF257510 BF065377 BE587679 WBF265236 I
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Hordeum vulgare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 749.
Location/Qualifiers
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Tel: 864 656 7288
Fax: 864 656 4293
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AUTHORS
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BF065825
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BF064990 HV_CED002
BF559387 HV_CED002
BF065067 HV_CED002
BF066058 HV_CED002
BF066058 HV_CED001
BE214473 HV_CED000
BE214577 HV_CED000
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2693.125 Million cell updates/sec
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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                          11351937 segs, 5372889281 residues
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Listing first 45 summaries
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/cultivar="C116151 (Mla6)"

Adb_xxef="texon:4513"
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/clone=lib="Hordeum vulgare seedling green leaf EST
library HVCDNA0005 (Erysiphe infected 5 control)"
/tissue_type="seedling green leaf"
/lab_nost="Solk"
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92.6%;
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/note="Vector: lambda2AP; Site_1: EcoR1; Site_2: Xho1; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 268 c 255 g 137 t
BF064990 824 bp mRNA EST 09-MAR-2001
HV_CEb0022F13f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CEb0022F13f, mRNA sequence.
BF064990.1 GI:10841629
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ta; Liliopsida; Poales; Poaceae; Pooideae
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Wing,R., Close,T.J., Kleinhofs,A., Wernodle,S., Palmer,M., Rambo
,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
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Contact: Wing RA
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Pred. No. 2.3e-110;
0; Mismatches 59; I
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library WroNa0005 (Erystphe infect
/tissue_type="seedling green leaf"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University
100 Jordan Hall, Clemson, SC 29634, US.
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
seq primer: AATTAACCCTOACTAAAGG
High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Institute
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/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Stre
Spermatophyta; Magnoliophyta;
; Triticeae; Hordeum.
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6 63	453 G 453 G 513 G	513 g	573 g 633 G	633 c - 693 C	693 c 753 C	RESULT 3 BE559387 LOCUS DEFINITION	CESSION RSION YWORDS URCE ORGANISM		REFERENCE AUTHORS	LE	JOURNAL COMMENT		RES	source		
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Hordeum vulgare
Hukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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HYCDM0005 (Erysiphe infected & control) Hordeum vulgare cDNA CED013H08f, mRNA sequence.
BF065694 GI:13265337
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                                                          2;
                                   Score 597.6; DB 10; Length 937; Pred. No. 2.3e-105; 0; Mismatches 74; Indels 2;
182
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264
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                                      77.5%;
89.7%;
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                                                        Matches 664; Conservative
280
                                              Similarity
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 211
                                       Query Match
Best Local 3
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gtgtccttcaggacggccatgtggttctggatgacggcgcagggaaacaagccgtcctgc
                                                                                        cacaacqtcqccctacqccqctggacqccqacqqccgccgacacaccgctgccggcagggta
                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HV_CED0022N01f"
/clone_lib="Hordeum vulgare
library HVcDNA0005 (Erysiphe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism~"Hordeum vulgare"
/cultivar="C116151 (Mla6)"
/db_xref~"taxon:4513"
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Seg primer: AATTAACCCTAAAGGG
High quality sequence stop: 589.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF065067.1 GI:10841706
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90.98;
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Unpublished (2000)
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Best Local Similarity
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AUTHORS
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
              Triticeae: Hordeum.

Triticeae: Hordeum.

(bases 1 to 923)

Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, Y., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                     Development of a genetically and physically anchored EST resource
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/organism="Hordeum vulgare"
/organism="Hordeum vulgare"
/doutivar-1016151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEb0013H08f"
/clone=lib="Hordeum vulgare seedling green leaf EST
library HYCDMA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ctgoccaaccgcgacaactcgctgtgcccggccagagggttctacaacgtacgacgccttc
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Unpublished (2000)
On Oct 17, 2000 this sequence version replaced gi:10842333.
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Pred. No. 9.5e-104;
0; Mismatches 93;
                                                                                                                                                                                                                                         100 Jordan Fall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                            Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 640.
Location/Qualiflers
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Llarity 87.2%;
Conservative (
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Contact: Wing RA
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BF065067 829 bp mRNA EST 09-MAR-2001
HV_CEb00022N01f Hordeum vulgare seedling green leaf EST library
HVCED0A0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BY_CEb0022N01f, mRNA sequence.
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1 (bases 1 to 829)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Wood, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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/hote="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To see http://www.genome.clemson.edu/orders" 247 c 270 g 167 t
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                                                                                                                                                                                                              659 ggaacgacgccaacgtcgaccgcatcgg---ctactacacgcgctactgcggcatgctcg
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                                                                                                                                                                                                                                                                                                                                                                                                  716 gcacggccaccggaggcaacctcgactgctacacccagaggaacttcg
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COMMENT Contact: Wing RA Clemson University Clemson University Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: wing@clemson.edu Seq primer: AATTAACCTTAAAGGG High quality sequence stop: 860. Location/Qualifiers 1. 936 Jordanism="Hordeum vulgare" /organism="Hordeum vulgare seedling green leaf EST /olone="Hordeum vulgare seedling green leaf EST /clone="Hordeum vulgare seedling green leaf" //db_xref="Hordeum vulgare seedling green leaf EST /clone="Hordeum vulgare seedling green leaf" //db_bost="seedling green leaf" //db_bost="seedling green leaf" //db_bost="seedling green leaf" //db_bost="sock" //db_bos	Query Match 73.7%; Score 568.6; DB 11; Length 936; Best Local Similarity 90.0%; Pred. No. 8.6e-100; Indels 10; Gaps 5; QY 1 atggggggggggggttggcgcgcgcgcgcgcgcgcgcgcg	Oy 301 gctgccgaccagttccagtggggctactgcttcaaggaagataagcaaggccacgtcc 360
QY 84 gggctcggtcatcacgcgtcggtcgttacgcgagcactctgcccaacgcgacaact 139 2; QY 84 gggctcggtcatcacgcggtcggtgtacgcgagcactctgcccaacgcgacaact 139 111 11 11 11 11 11 11 11 11 11 11 11 11	QY 440 acctggtgagcaacccagacctagtgtccacggacggtgttccttcaggacggcca 499 DD 385 ACCTGTGAGCAACCGGATCTGGTGCCACGGAGGGGGGTGTCTTCAGGACGCGGA 326 QY 500 tgtggttctggatgacgacacagggaaacaagccgtcgtcgTCTTCAGGACGCCGAGGGCAACGTCGCCTACGCCTACGCCTACGCCTACGCCTACGCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACGCCCTACACGCCCCTACGCCCTACACGCCCCTACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACACGCCCCACCA	BEFOREOUS BFO66058 BF

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/lab_lost="TyCl2"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
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HV-CDE0009J09f Hordeum vulgare seedling green leaf EST library
HYCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV-CE00009J09f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                 -cat 710
                                                                751 cegaaceacecccaacercaarcecrieserracraacacececracrescegesaarre 810
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Onpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11195492.
Contact: Wing RA
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                                 658 eggaacgaeg-ceaaegtegaeegeateggetaetaeaegegetaetgegg-
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Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University
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Seq primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
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                                                                                                                                       811 GCTCGGCACGGCCACCGGGGG 831
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Eukaryota; "Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 669)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saki, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
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HV_CEb0006000f Hordeum vulgare seedling green leaf EST library
HV_CED00005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BE21473
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543 ATGGGGCCGGACGACGCCAACGTCGATCGCATCGGGTACTACACGCGCTACTGCGGGATG
                                                                                                                 472 gacgcggtggtgtccttcaggacggccatgtggttctggatgacggcgcagggaaacaag
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Clemson University
100 Jordan Hall, Clemson, SC 29634, US
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/cultivar="C116151 (Mla6)"
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 644.
Location/Qualifiers
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Fax: 864 656 4293
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On Jul 3, 2000 th
Contact: Wing RA
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Best Loca Matches

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BASE COUNT ORIGIN

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                            Spermatophyta; Magnoliophyta;
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91.9%;
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HV_CED50003NL9f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BE214577
                                                                                         For
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                                                                                                   more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To sorder a clone see http://www.genome.clemson.edu/orders" 223 c 214 g 107 t l others
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/tissue_type="seedling green leaf"
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Pred. No. 2.3e-95;
0; Mismatches 42;
/db_xref="taxon:4513"
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ilarity 93.1%;
Conservative 0
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ACCESSION VERSION KEYWORDS

SOURCE

BE214577

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library HVcDNA0005 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="Solk"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                      Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, X., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
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227 c 218 g 116 t 1 others
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                                                                                                                                                                                                                 Development of a genetically and physically anchored EST
                                                                                                                                                                                                                                        for barley genomics
Uppublished (2000)
On Jul 3, 2000 this sequence version replaced gi:8902189
Contact: Wing RA
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pred. No. 4.7e-94; 
0; Mismatches 50; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288
Fax: 864 656 4293
Email: rwingeclemson.edu Seq primer: AATTAACCCTCACTAAAAGGG High quality sequence stop: 638.
Location/Qualifiers
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HV.CED0003A01f Hordeum vulgare seedling green leaf EST library
HV.CDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BE214283
                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 725)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/Parley/ To see http://www.genome.clemson.edu/orders" 226 c 211 g 123 t
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/organism="Collivar="Cifols" (Mla6)"
/db_xref="taxon:451" (Mla6)"
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/clone=lib="Hordeum vulgare seedling green leaf EST library HyconA0005 (Brysiphe infected & control)"
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/lab_host="SouR"
                                                                                                                                       616 CGCIGCCGATACAGCIGCAGGTCGGGGGGGATACGGCGGTATCACCAATATCATCAA
                                                                      573 ggccgccgacaccgctgccggcagggtacccggatacggagtgatcaccaatatcatcaa
gacggcgcagggaaacaagccgtcgtgccacaacgtcgccctacgccgctggacgccgac
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Pred. No. 3.6e-91;
0; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC 29634, USA
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Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
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Seq primer: AATAACCTCACATAAGGG
High quality sequence stop: 670.
Location/Qualiflers
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2 CCGGGCTTCGGCACCACCGCCAGCGCCGTTGACATCAAGCGCGAGCTCGCCGCCTTCTTC 61

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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 713)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodie, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
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                                      62 GCCCAGACCTCCCACGAGACCACGGAGGGACGAGGCGCCGCCGACCAGTTCCAATGG 121
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ggccagacctcccacgagaccaccggagggacgagaggggcgctgccgaccagttccagtgg
                                                                                                                                                                                     for barley genomics
Unpublished (2000)
On Dec 19, 2000 this sequence version replaced gi:11892815.
Contact: Wing RA
Clemson University Genomics Institute
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/organism="Hordeum vulgare"
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Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 703.
Location/Qualifiers
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100 Jordan Hall, Clemson,
Tel: 864 656 7288
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BF628657.2 GI:13090309
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Hordeum vulgare
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HV_CED0009C12f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CED0009C12f, mRNA sequence.
BE216024.1 GI:8903636
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                          EST library
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                                                                                                                                                                                                                                                                                                                               153 cagagggttctacacgtacgacgcettcatcgccgccaacacettcccgggcttcgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 acccagacctagtgtccacggacgcggtggtgtccttcaggacggccatgtggttctgga
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                                                                                                                                                                             Length 713;
                      /clone_lib="Hordeum vulgare seedling shoot
HVcDNA0002 (Debydration stress)"
/tissue_type="Seedling shoot"
/lab_host="TyCl21"
                                                                                                                                                                 Score 511.6; DB 11; Luc. 2. Pred. No. 7.2e-89; Indels
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/db_xref="taxon:4513"
/clone="HVSMEb0006P01f"
                                                                                                                                                                            66.4%;
89.0%;
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Bukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta, Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
1 (base; Hordeum.
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu.Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Wood, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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/tab_host="SoLR"
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Pred. No. 7e~86;
0; Mismatches 26;
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="C116151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CED0009C12f"
/clone_lib="Hordeum vulgare
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/organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                              Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAGGG
High quality sequence stop: 581.
Location/Qualifiers
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95.28;
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Unpublished (2000)
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Best Local Similarity 95.2
Matches 511; Conservative
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Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 522.
Location/Qualifiers
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Fax: 864 656 4293
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1 (bases 1 to 923)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu.Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo Wood,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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af EST library
vulgare cDNA clone
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466 GGGAGAGCGATCGGGAAGGACCTTGTGAGCAACCCGGATCTGGTGTCCACGGACGCGGTG
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Pred. No. 9.7e-86;
0; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SC 29634, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 811.
Location/Qualiflers
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BF266125 576 bp mRNA BST 09-MAR-2001
HV_CEa0014D24f Hordeum vulgare seedling green leaf EST library
HYCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HY_CEa0014D24f, mRNA sequence.
BF266125. GI:13262558
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Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
'Triticeae; Hordeum.
I (basea I to 576)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo Wood,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
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On Nov 17, 2000 this sequence version replaced gi:11197119.

Contact: Wing RA Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                     360
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gotgoogaccagttccagtggggctactgcttcaaggaagagataagcaaggccacgtcc
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AUTHORS
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HV_CEa0013NO9f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HY_CEa0013NO9f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
                                                                                                                                                                                                                                                         H
                                                                                                                   /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
                                                                                                                                more details on library preparation and sequence analysis see http://www.genome.cleanson.edu/projects/barley/ To see http://www.genome.cleanson.edu/orders" 184 c 185 g 101 t 2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      363 GCCGCCGACCAGTTCCAATGGGGCTACTGCTTCAAGGAAGAGTTAGCAAGGGCACGTCT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ccaccatactatggacgggacccatccaattgacagggcggtccaactacgatcttgcc 420
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library HvcDNA0004 (Erysiphe infected & control)"
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/lab_host="TJC121"
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         /organism="Hordeum vulgare"
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Similarity 92.4%;
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Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu, Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 184 c 1977 g 95 t.
                                                                                                         EST resource
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Unpublished (2000)
On Nov 17, 2000 this sequence version replaced gi:11196972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    // Organism="Hordeum vulgare"
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Pred. No. 5.1e-74;
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                                                                                                                                                                                                                                   Clemson University Genomics Institute
Clemson University
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
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93.2%;
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549 GACGGCCCAAGGCAACAAG 567

Search completed: May 3, 2002, 16:23:53 Job time: 7193 sec

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3, 2002, 15:34:10 ; Search time 3990.51 Seconds (without alignments) 4018.348 Million cell updates/sec
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1 atgtccacgctgagaggggg.....ttggggctcgcgggacatgga 972
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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SUMMARIES

Description	X55787 O.sativa L. L34211 Hordeum vul L37289 Oryza sativ AF000966 Poa prate AF009966 Poa prate AF280437 Secale ce	U02286 Oryza sativ V02287 Hordeum vul AB051287 Secale ce AF000964 Poa prate D16223 Rice Cht-3 AP0003685 Oryza sat D16221 Rice Cht-1 I84465 Sequence X56063 O.sativa mR X54367 Oryza sativ	X87109 O.sativa (P X87109 O.sativa RC M62904 H.vulgare L A37990 Sequence 9 AR03757 Sequence 9 I75200 Sequence 9 I34210 Hordeum vul AB051579 Secale ce D16222 Rice Cht-2 AB018248 Oryza sat AB012855 Oryza sat AB012855 Oryza sat AB013868 P.vulgaris M13968 P.vulgaris VAB30751 Vigna ses	Z29962 O. Sativa (P. 100973 Zea mays ac \$43926 CH5B=chitin AB018655 Cucurbita AB048651 Psophocar E13289 CDNA encodi E13289 CDNA encodi E13299 CDNA encodi I23881 Sequence 1 I16798 Zea mays cl Info Control Co	PLN 05-MAY-1995 a; Embryophyta; Tracheophyta; ida; Poales; Poaceae; and Hibi,T. ession and chromosomal	
A	OSLMRNAC BLYCH133A RICCHITA AF000965 AF000966	OSU02286 PACHIG HVU02287 AB051578 AF000964 RICCHT3 AP003685 RICCHT1 184465 OSENDO	OSCHITIA OSDNARC24 BLYCHI A37990 A37990 A37990 A175200 BLYCHI26A ABO11279 ABO11855 ABO11855 PHYCHM PHYCHM ABO11855 PACHII PHYCHM	OSCHITIB NZECHITIB NZECHITIC SA4926 AB015655 AB0148531 E13289 E13290 I23881 I23881 I22381 RZECHITINA ALCCHINITA PERCHIZI HBR238579	ALIGNMENTS 1186 bp mRNA ### for endochitinase. ### ### ### ### #### #### ##########	
Length DB	186 8 779 8 291 8 173 8 080 8	051 8 9985 8 684 8 191 8 2552 8 808 8 739 8 739 8 151 6 237 8	2000 100000 88 88 88 88 88 88 88 88 88 88 88 8	80077288888888	1186 bp GI:407471 ase. Var. va. va. viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan viridiplan	1
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LHRNDGACPARGFYTYEAFLAAAAAFPAFGGTGNTETRKREVAAFLGGTSHETTGGWP
                                                                                                                                                                                                                                                     TAPDGPFSWGYCFKOBONPPSDYCOPSPEMPCAPGRKYYGRGPIQLSFNFNYGPAGRA
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                                                                                                                                                                                                                       /translation="MSTPRAAASLAKKAALVALAYLAAALATAARAEQCGAQAGGARC
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Direct Submission
Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
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Pred. No. 1.2e-71;
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                                                                                                           /clone="RCC2"
10. .105
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1057. .1062
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Hordeum vulgare
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae,
Pooldeae, Triticeae, Hordeum.
1 (bases 1 to 1779)
Leah, R., Skriver, K., Knudsen, S., Ruud-Hansen, J., Raikhel, N.V. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       099
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Identification of an enhancer/silencer sequence directing the aleurone-specific expression of a barley chitinase gene 95078949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLYCHI33A 1779 bp DNA PLN 29-NOV-1994
Hordeum vulgare chitinase (CHI33) gene, complete cds.
L34211
aagcaggagcagggctcgccgccgagctactgcgaccagagcgccgactggccgtgcgca
                         cccggcaagcagtactatggccgcggccccatccagctcacccacaactacaactacgga
                                                                                                                coggocgogogaatcggggtggacctgctgaacaatccggacctggtggccacggac
                                                                                                                                                                                                         CCGGCGGGGAGGCCATCGGGTGGACCTGCTGAACAACCCGGACCTGGTGGCGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  cgggtacccgggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatg
                                                                                                                                                                                                                                                                  cogacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaacaagccg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           On Nov 28, 1994 this sequence version replaced gi:507960.
Location/Qualifiers
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/tissue_type="seed"

614...620

682...1680
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682. .1680
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DAACPARGEYTYDAFVTAAAAFPDFAATGDDEARKREVAAFLGGTSHETTGGWATAPD
GPSKWYCKRELAAAASVCYASAEWPCAADKKYFGROLDGSYNWYDAGAGEDGED
LLNNPELYASDPVVSEKTALWFWMTPOSPKSCHDVITGOWTPSSODIAAGRYPGYGY
ITNIINGELEGGFGPDDRVANRIGFYQRYCDVLGIGYGSNLDCYDQRPFNSGLAAVQ"
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GWCGSTSDYCGDGCQSQCDGCGGGGGGGGGGGGGGAVEAVSKELFEQLLLHRN
                                                                                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
     1597 GGCGTCGCTACGGGGGCAACCTCGACTGCTACAACCAGAGGCCCTTCGTCGAGGGGCTT 1656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /function="chitinolytic activity, antifungal activity"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56 CGACAGCAGTGGCCCTCCTCGTGGCCGCGCCCATGCTGGCGCCAGGTAGTCGCCGAGC 115
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                                                                                                                                                                                                                                                                                                                                                             Organ sativa
Organ sativa
Divaryota: Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaces
Ehrhartoideae; Oryzeae; Oryza.
I (bases 1 to 1291)
Yun,C.-H., Kim,J.-K. and Park,Y.-H.
Isolation and Characterization of A Rice Chitinase CDNA
Unpublished (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39;
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Pred. No. 1.5e-68;
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/protein_id="Aaa56787.1"

/db_xxef="G1:507961"

/tanslation="ARGPSVVARAUAIVLSAALAMAWVRAQQCGSQAGGATCPNCLC
CSRFGYKGSREDYCAGAGQSQCSGCGPPPPGBPGGGYSSIISRDLFEGFLHRDRCD
DAGGYTYDAFLAAATFPARGTTGSTEIRRQEVAAFFGGTSHETTGGWAITAPDGFYS
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PDLVANDATVSSPIALWFWAFFGDANKPSSHAVITGGWTPAADTAAGRVPGTGVITWI
INGGLECGRGADSRYADRIGFYQRYCNILGVGYGGNLDCTNQRPFVEGLLIQRVTE"
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Pred. No. 7.4e-69;
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1 (bases 1 to 1173)
Du.M. and Ha.S.B.
Direct Submission
Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley, 94706, USA

AUTHORS

JOURNAL

/organism="Poa pratensis" /strain="Glade" /db_xref="taxon:4545"

194. 346 /gene="Chi3" 194. 346 /gene="Chi3" /note="chitinase"

Location/Qualifiers 1. .1173

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Score 561.2; DB (Pred. No. 1.2e-67) 0; Mismatches

57.78; 76.38;

Local Similarity 76.3 nes 714; Conservative

Best Loca Matches

Query Match

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/codon_start=1

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215 GCCATGCTGGTGGGGCCTTCGCGGTGTCTGCACGCGGAGCAGTGCGGGCTAGCAGCAGCAGTGCGGGCTAGCAGCAGTGCGGGCTAGCAGGCAA

43 gtcgtcctggcggcggcgggtcacgccggccacggccgagcagtgcggctcgcaagcc

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394 258 gcettettggecgecggeggggggtteccggeetteggcaccaceggagacetggacaeg 515 GCCTTCGTCGCCGCCGCCAACTCTTTCGCCGGCTTCGGGACCACGGGCGGCGCACCGAC

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ggccgcgggccccatccagctcacccacaactacaactacggaccggcggcggcatc 618

31-0CT-1999 DNA PLN 3 (Chi3) pseudogene sequence. Poa pratensis chitinase AF000965

AF000965.1 GI:6164586 ACCESSION VERSION KEYWORDS

DEFINITION

Kentucky bluegrass. ORGANISM

Poa pratensis Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnollophyta; Lillopsida, Poales, Poaceae, Pooideae, Triticeae,
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Yeh,S., Moffatt,B., Griffith,M., Xiong,F., Yang,D.S.C.,
Wiseman,S.B., Sarhan,F., Danyluk,J., Xue,Y.Q., Hew,C.L.,
Doherty-Kirby,A. and Lajoie,G.
Chitinase genes responsive to cold encode antifreeze proteins in winter cereals
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Secale cereale 31.7 kDa class I endochitinase-antifreeze protein
precursor, mRNA, complete cds.
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GTTSDXCGTGCQSQCNGCSGPTPVTPPSGGGGVSSIVSQSLFEQMLLHRNDAACLAK
GFYTVAAFIAAANSFAGFGTTGSTDVEKREVAAFLAQTSHETTGGWFTAPDGPYSWGY
GFYQEQGATTAPANSFAGFGKKYFGRGPTQISTWYNTGPAGQATQTDLINNPDL
VATDPFVSFKXALMFWMTAQSPKPSSHAVITGGWSFSSADQAAGFVPGGVTVINING
GLECGKGQDNRVADRIGFYKRYCDLLGVSYGNNLDCYSQRPFGS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Poa pratensis, Bukaryota, Embryophyta; Encheophyta; Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Poace; Pooldeae; Poace; Pooldeae; Poace; Pooldeae; Poace; Pooldeae; Poace; Pooloe; Pooloe;
                                                                                                                                                               995 GIGALCACIAACAICAICAACGGGGGGCTCGAGIGCGGCAAGGGGCAGGACAACGGGTC 1054
                                                                                                                                                                                                                                                                          1055 GCCGACAGGATCGGGTTCTACAAGCGCTACTGCGACCTCCGGCGTCAGGCTACGGGGAC 1114
                                                                                                                                                                                                                         gcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggctacgggaat 918
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     acggggctgtggactccgacggccagggatagcgcaggccggacgggtacccgggtatggt 798
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                                                                                                              gteateaceaacgteateaacggegggateeaatgeggeatggggeagaacgacaaggtg
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                                                    27;
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Pred. No. 1.6e-66;
0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                 aacctcgactgctacaaccaattgtcgttcaacgtt 954
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/codon_start=1
/product="chitinase"
/protein_id="AAR04454_1"
/db_xref="GI:6164588"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="Glade"
/db_xref="taxon:4545"
28. .990
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75.6%;
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28. .990
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                                                                                                                                                                                                                                                                                                                       /translation="MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFC
GSTSBYCGGAGGACQSQCBNCGGSTPVPVPAPTGGGVSSISQSCHFPDQMLIANDAACLAKG
GSTSBYCGAGAANGSTPVAMTNDAARLAQUSHETTGGWPTAPDGFYSWGYC
FVNQAFIAAANSFSRATGGTDVRKREVAARLAQUSHETTGGWPTAPDGFYSWGYC
FVNQAFGAPSDYCSPSSQWPCAPGKKYFGRGPIGISYNVNGPAGRAIGTDLLNNPDLV
ATDATVSFRALWFWMTPQSPKRSSHDVITGFWSPSGADQAAGRVPGYGVITNIINGG
1889 C
389 C
204 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 ACCGACGTCAGGAAGGGCGAGGTGGCCGCGTTCCTAGCTCAGGACCTCCCACGAGACCACC
                           Tobacs 1 to 1192)
Yeh, S., Moffatt, B., Griffith, M., Xlong, F. and Hew, C.L.
Direct Submission
Submitted (20-10N-2000) Biology, University of Waterloo, University Ave West, Waterloo, ON N2L 3G1, Canada
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 543.4; DB 8;
Pred. No. 3.2e-65;
0; Mismatches 211;
   Plant Physiol. 124 (3), 1251-1264 (2000)
                                                                                                                                     /organism="Secale cereale"
                                                                                                                                                                                                                                                                                          /protein_id="AAG53609.1"
/db_xref="G1:12407647"
                                                                                                                                                   /variety="Musketeer"
/db_xref="taxon:4550"
                                                                                                                                                                                                                                                                                 protein precursor"
                                                                                                                                                                                     /chromosome="1"
                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.9%;
75.0%;
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PNCLCCSRWGWCGSTSDFCGDGCQSQCSGCGPTPTPPSPSGGVGSIVPRDLFERLLLH
RNDGACRAAGFYTYEAFLRRAAFPAFGGTGDJTSTRKREVAAFLGQTSHETTGGWPTAP
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DLLSNPDLVATDATVSFKTALWFWMTPQGNKPSSHDVVTGRWAPRRDVAAGRAGYGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryza.

1 (bases 1 to 1051)
Anuartha; C.S., Mew,T. and Muthukrishnan,S.
Induction of Chitinases and beta-glucanases in Rhizoctonia solani infected rice plants: Isolation of an infection-related chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheophyta;
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                                           cgcgcaatcggggttggacctgctgaacaatccggacctggtggccacggacccgacagtg
                                                                               661 CGGGCCATCGGCACGGACCTACTCAACAACCCAGACCTCGTGGCCACGGACGCCACGTG
                                                                                                                                                                                                          gacgtgatcacgggggctgtggactccgacggccagggatagcgcagccggacgggtaccc
                                                                                                                                                                                                                                                                                        gggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgggggaac
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Oryza sativa IR58 chitinase mRNA, complete
U02286
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/clone="clone RC-7"
/tissue_type="leaf"
/clone_lib="lambda GT11"
/dev_stage="mature"
1.1051
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/db_xref="G1:495303"
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/organism="Oryza sativa"
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/EC_number="3.2.1.14"
/function="hydrolyzes
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Muthukrishnan, S.
Direct Submission
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TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                       27;
                                                                                                                                                                                                                                                                                                                  Length 1051;
                                                                                                                                                                                                                                                                                                         Score 537.6; DB 8; Length. Pred. No. 2.1e-64; 0; Mismatches 204; Indels
                                            // 1018
/partial
/Ec_number="3.1.2.14"
/function="hydrolyzes chitin"
/product="chitinase"
a 370 c 378 g 139 t
                                                                                                                                                                                                                                                                                                      55.3%;
75.9%;
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                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 75.9
Matches 727; Conservative
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                          sig_peptide
mat_peptide
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YCFNQERGAASDYCSRNGQWPCAPGKKXFGRGPIQISYNYNYGPAGRAIGTDLINNPD
LVAIDATVSFKTALWFWMTPQSPKPSSHDVITGRWSPSGADQAAGRAIGTDLINNIN
                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (09-NOV-1993) Y. Liao, Inst. fuer Biologie I, RWTH,
Worringer Weg, 52056 Aachen, FRG
2 (bases 1 to 1985)
Liao,Y.C., Kreuzaler,F., Fischer,R., Reisener,H.J. and Tiburzy,R.
Characterizaiotn of a wheat class Ib chitinase gene differentially
induced in isogenic lines by infection with Puccinia graminis
plant Sci. 103,177-187 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooldeae, Triticeae, Triticum.
884 GACGACCGCGTGGCAAACCGGATCGGCTTCTACCAGGCCTACTGCGGGCGCGTTCGGCATC 943
                                                                      1001
                                                                                                                                                           02-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                              30;
                                                                                                                                                   T.aestivum (Chinese spring) chi gene for endochitinase.
X76041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGLECGRGQDGRVADRIGFYKRYCDLLGVTYGDNLDCYNQRPFA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .1985
Organism="Triticum aestivum"
/cultivar="Chinese spring"
/db_xref="taxon:4565"
/clone_lib="lambda gem-12 genomic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 537.4; DB 8;
Pred. No. 1.7e-64;
0; Mismatches 211;
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554 c 552 g 41
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71. .75
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/gene="CHI"
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                GIGGIGGIGGCCATGCCGCGCGCCTTCGCCGTGTCTGCGCACGCCGAGCAGTGCGC
                                                                                                                                                              244 agggacctettcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcggg
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                                             tegeaageeggegeeaagtgegeegaetgeetgtgetgeageeagttegggttetge
                                                          ggcaccacctccgactactgcggcccccgctgccagagccagtgcactggctgcggtggc
                                                                                                            --eggoggoggggtggcctccatogtgtcc
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gtoctggccgtcgtcctggcggcggcggcggtcacgccggccacggccgagcagtgcggc
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30-MAY-1994

HVU02287 1684 bp DNA PLN 30-MAY-1994 Hordeum vulgare cultivar NK1558 chitinase gene, complete cds. U02287

GI:495304

U02287.1 barley

VERSION KEYWORDS

SOURCE

DEFINITION ACCESSION

HVU02287 RESULT

rocus

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FKQERGATSNYCTPSAQWPCAPGKSYYGRGPTQLSHNYNYGPAGRATGVDLRNPDLV
ATDPTVSFKTAMWFWMTAQAPKPSSHAVITGQWSPSGTDRAAGRVPGFGVITNIVNGG
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Spermatophyta; Magnoliophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 1684)
Ignatius, N.J., Huang, J. and Mnthubrita.
                                                                                                                                                                                                                     clone
                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (29-SEP-1993) Muthukrishnan S., Kansas State University,
Biochemistry, Willard Hall, Manhattan, KS 66560, USA
Location/Qualifiers
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600. .656
657. .1553
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Pred. No. 2.5e-64;
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/organism="Hordeum vulgare"
/strain="cultivar NK1558"
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/clone="clone 61N"
/tissue_type="leaf"
/clone_lib="lambda gr11"
/dev_stage="seedling"
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/function="hydrolyzes
/product="chitinase"
514 c 471 g
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/function="hydrolyzes
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Muthukrishnan, S.
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
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                       CACCACCGGCGGCACCCGGACACCGGCGAGGTGGCCGCCTTCCTGGCCCAGACCTC
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Pooideae, Triticeae, Secale.
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Chnuma, I., Yamagami, I. and Ishiguro, M.
Cloning and Sequencing of the Rye Seed
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Ohnuma,T., Yamagami,T. and Ishiguro,M.
Direct Submission
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58. .1023
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/translation="WGAFALEAVLAWAYTWAVAEQCGSQAGGATCPNCLCCSRFGWCG
STSDYCGDGCQSCCAGCGGGGTPVTPTPTPSGGGGVSIVSRALFDRMLLHRNDGACQ
AKGFYTYDAFVAAAGAFPGFGTTGSTDTRKREVAAFLAQTSHETTGGWATAPDGAFAW
                                                                                                                 GYCEKQERGATSNYCTPSAQWPCAPGKSYYGRGPIQLSHNYNYGPAGRAIGVDLLRNP
DLVATDPTVSFKIAMWFWMTAQAPKPSSHAVITGQWSPSGTDRAAGRVPGFGVITNIV
NGGIECGHGQDSRVADRIGFYKRYCDILRVGYGNNLDCYNQRPFA"
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Pred. No. 3.3e-64;
0; Mismatches 210; Indels 3
/product="seed chitinase-a"
/protein_id="BAB18519.1"
/db_xref="G1:11344587"
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Du,M. and Ha,S.B.
Direct Submission
Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley,
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Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko
Nishizawa. National Institute of Agrobiological Resources, Rice
Genome Research Program; 2-1-2 Kannondai, Tsukuba, Ibaraki 305,
Japan (E-mail:CS.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
Submitted (11-MAY-1993) to DDBJ by:
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                                                                                                                                                367 gacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacgagacc 426
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                                                tacacgtacgacgccttcttggccgccggcggcggcgttcccggccttcggcaccaccgga
                                                                                                                                                                                                                                                                                 460 ACCGGCGGGGGGCGACGGCCCCGACGGCCCCTACTCCTGGGGCTACTGCTACAAACAG
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endochitinase.
Cryza sativa (strain Nipponbare) DNA, clone RCG3.
Oryza sativa
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Rice Cht-3 gene for
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2655

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Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakidabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-3874441, Fax:81-298-387468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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2236 TGGCGCAGACGTCCCACGAGACCACCGCGGCGCCCCACGGCCCCGACGCCCCTACT 2295
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                                                                                                                              521 gegecgaetggeegtgegeaceeggeaageagtaetatggeegeggeeceateeagetea
                                                                                                                                                                   2356 AGCCGGAGTGGCCGTGCGCCGCCGCCAGAAGTACTACGGCCGGGGACCCATCCAGATCA
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Oryza satiya nipponbare(GA3) genomic DNA, chromosome 6,
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Ehrhartoideae; Oryzeae; Oryza.
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KEENNGNAPTYCEPKPEWPCAAGKYFYGRGPIQITYNYNYGPAGQAIGSDLLNNPDLV
ASDATVSFKTAFWFWATPQSPKPSCHAVITGGWTPGADDQAGRYPGTGEITNIINGG
VECGHGADDKVADRIGFYKRYCDMLGVSYGDNLDCYNQRPYPPS"
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/evidence=experimental
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/gene="Cht-3"
/EC_number="3.2.1.14"
               Institute of Agrobiological Resources
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/db_xref="G1;500617"
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/db_xref="taxon:4530"
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the accession number will be preserved.
Location/Qualifiers
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/organism="orgas sativa"
/cultivar="Yipponbare"
/db_xref="taxon:4530"
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YCKEBNINGYGSDYCYQSOWPCAGKKYYORGPQIGSRILSN
PDIVAASDATYSFKIREWWIPOSPKPSCHAYMTGQWTPNGNDQAAGRYPGYGYTNI
INGGVECGHGADSRVADRIGFYKRYCDMLGYSYGANLDCYNQRPFNS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (sub_species japonica, strain Nipponbare) DNA, clone
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Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko
Nishizawa, National Institiute of Agrobiological Resources, Rice
Genome Research Program: 2-1-2 Kannondal, Ishkuba, Ibaraki 305,
Japan (E-mail:CS.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
Submitted (11-MAY-1993) to DDBJ by:
                                                                                                     19230 GCGGTGTGGAGTGCGGGCACGCGCGGACGACGTGGCCGACCGGATCGGGTTCTACA 19171
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1 (bases 1 to 2739)

1 (bases 1 to 2739)

1 (bases 1 to 2730)

1 (bases 1 to 2730)
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Tsukuba, Ibaraki 305
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/evidence=experimental
1318. .2289
/gene="Cht-1"
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/product="endochitinase"
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Location/Qualifiers
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Pred. No. 1.5e-59;
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/gene="Cht-1"
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ACATGITGGGGGCGCAACTIGGACTGCAACTACAACAACAAGAGGCCTTTCAAC
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Phu'Q. and Lamb,C.J.
Plant defense genes and plant defense regulatory elements
Patent: US 5695939-A 2 09-DEC-1997;
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Pred. No. 7.5e-59;
0; Mismatches 234;
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Best Local Similarity 72.4%;
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Search completed: May 3, 2002, 15:36:53 Job time: 4502 sec

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3, 2002, 16:32:02 ; Search time 309.71 Seconds (without alignments) 2690.647 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	*********************	Rye chitinase-like	RCH10 chitinase qe	Rice chitinase RCH	Nucleotide seguenc	CDNA encoding a ma	Sequence encoding	Floral organ-speci	Sequence encoding	Chitinase coding s	Full length chitin	American elm chiti
SUMMAKLES			ID		AAX24889	AAQ31408	AAQ81346	AAF54983	AAA96224	AAQ62518	AAV49982	AA005264	AAT79940	AAT79941	AAT33325
			DB	1 1	20	13	16	22	21	15	19	11	18	18	17
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	æ	Query	Match	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	55.9	51.1	51.1	51.1	50.8	48.3	42.8	40.8	38.6	38.6	38.1
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ALIGNMENTS

RESULT

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CHT9; chitinase-like protein; antifreeze protein; AFP; winter rye; antifungal; fungicide; cold tolerance; frost tolerance; transgenic plant; preservation; cryopreservation; tumour; therapy;
                                                                                                                                                              Location/Qualifiers
1..954
7.4tag= a
7.00te= "separately claimed in Claim 2"
1..60
7.tag= a
61..954
7.ttag= b
                                                                                                                                                                                                                                              /note= "separately claimed in Claim 2"
                                                                       Rye chitinase-like protein CHT9 cDNA clone ch-9.
           AAX24889 standard; cDNA; 954 BP
                                                                                                                                                                                                                                                                                                            98WO-CA00745.
                                                                                                                                                                                                                                                                                                                               97US-0903872.
                                                  21-JUN-1999 (first entry)
                                                                                                                                            Secale cereale
                                                                                                                                                                                                                                                                    W09906565-A2
                                                                                                                                                                                                                                                                                                           31-JUL-1998;
                                                                                                                                                                                                                                                                                                                               31-JUL-1997;
                                                                                                                                                                                                         sig_peptide
                                                                                                                                                                                                                                                                                       11-FEB-1999
                                                                                                                                                                                                                              mat_peptide
                               AAX24889;
AAX24889
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The present sequence encodes winter rye (Secale cereale L. cv. Muskateer) CHT9 preprotein (see AAW98079). Mature CHT9 (see AAW98080) is a chitimase-like protein that has chitimase (antifungal) and antifreeze activities. CHT9 cDNA (ch-9) was obtained by isolating mana from rye plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitimases with antifreeze activity would be expressed, and then sorting the cold-induced chitimase cDNAs to determine which encoded proteins with ice-binding ability. CHT9 and CHT46 (see AAW98081-82) corting the cold-induced chitimase cDNAs to determine which encoded proteins with ice-binding ability. CHT9 and CHT46 (see AAW98081-82) corting the cold-induced chitimase cDNAs to determine which encoded proteins and in Arabidopsis thaliana. The chitimase-like antifreeze proteins can be used: to increase freezing tolerance of plants and microorganisms; to increase field survival of plants, animals and microorganisms exposed to sub-zero temperatures; to inhibit ice crypteservation and hypothermic protection of cells, embryos, tissues etc. (particularly human plantelets) is and too kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage caused by low temperature pathogens (particularly fungi) in plants, frozen foods and any cryopreserved
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                                                                                                                                                         New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gtoctggccgtcgtcctggcggcggcgggtcacgccggccacggccgagcagtgcggc 93
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                                                              Xiong F;
                                                                                                                                                                                                                                                                Claim 2; Fig 21a; 118pp; English.
                                                            Moffatt B,
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                                                                                                 WPI; 1999-153795/13.
P-PSDB; AAW98079, AAW98080.
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                   (ICEB-) ICE BIOTECH INC
                                                            Hew C,
                                                        Griffith M,
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                                                                                                                                                                                                                                                                             gacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggc 909
                                                                                                                                                                                                                                                                                                                                       912
                                                                                                                                                                         gogttcaagacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccat 729
                                                                                                                                                                                              673 tcatttaagacggcactgtggttctggatgacgccgcagtcaccaaaaccttcgagccac 732
                                                                                                                                                                                                                                            gacgtgatcacgggccggtggagcccctcgggcgccgaccaggcagcgggtagggtgcct 792
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/note= "Region conserved between class I and class
II chitinases"
                                                                                          cagggetegeegeegagetactgegaecagagegeegactggeegtgegeaeceggeaag
                                                                                                                                                                                                                                                                                                                                    853 getegtgtegeegacegaategggttetacaagegetactgtgaeeteeteggegteage
                                                                                                                                                                                                                     gacgtgatcacgggggctgtggactccgacggccagggatagcgcagccggacgggtaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Promoter; region; rice; chitinase; physical; biological; stress;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "Putative polyadenylation signal"
1093..1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= c
/note= "Putative polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                          tacgggaataacctcgactgctacaaccaattgtcgttc 948
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1053..1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RCH10 chitinase gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
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The sequence given represents the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this gene in mature plants is characteristic. There is a low level of expression in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyledon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant
                                                                                                                                       DNA fragment contg. chitinase gene and its regulatory region - is responsive to mature plant stress and has low level expression in leaves, moderate level expression in stem and high level expression in roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1151 BP; 197 A; 409 C; 353 G; 192 T; 0 other;
                                                                                                                                                                                                                                 Disclosure; Page 33-34; 45pp; English.
                BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                                                                                                                                                                                defence genes and selectable genes.
                                                                                      WPI; 1992-415785/50.
               (SALK ) SALK INST
                                                                                                     P-PSDB; AAR29019
                                                  Zhu Q;
                                                  Lamb CJ,
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Gaps 27; Length 0; Mismatches 234; Indels DB 13; Score 496.6; DB 13 51.1%; 72.4%; Local Similarity '2.* hes 684; Conservative

200 236 57 gagagogotogotgiggiggiggiggiggocaggocottootogoggoggoggogtgoatgo 116 cgagcagtgcggctcgcaagccggcggcgaccaagtgcgccgactgcctgtgctgcagcca 140 80 9ttcgggttctgcggcaccacctccgactactgcggccccgctgccagagccagtgcac 117 cgagcagtgcggcagccaggccggcggcggcggtgtgccccaactgcctctgctgcagcca 177 gttcggctggtgcggctccacctccgactactgcggcgccggatgccagagccagtgctc δ g

236 -----tggctgcggtggcggcggcggggtggcctccat 201 QQ $\Delta \alpha$

cgtgtccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggc 237 297

δy Q QYg

237 geggetgeggeggeggeeggeeggegteeggeggeggegtggeageggegtegegteeat

357 cagcaacttetacacetacgacgecttegtegeegeegeegeegteecteeegggettege 416 ccgcggggttctacacgtacgacgccttcttggccgccgccggcggcgttcccggccttcgg 297

caccaccygagacctygacacycygaagcygygaggtyggcygccttcttcygccagacctc 416 357

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ettcaagcaggagca---gggctcgccgagctactgcgaccagagcgccgactggcc 477 ccacgagaccaccggcgggtgggcgacggcgcccgacggcccctacacgtggggctactg 477

536

9t9c9caccc9gcaagcagtactatg9ccgcggccccatccagctcacccaccaactacaa 537 cttcaaggaggagaacggcggcggcgggccggactactgccagcagagcgcgcagtggcc 534

gtgcgccgccggcaagaagtactacggccggggtcccatccagctctcctacaacttcaa

597

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Qγ

ctacgggccggcggggcaggccatcggcgacctgctcggcgacccggacctcgtggc 716 ctacggaccggcggcgcaatcggggtggacctgctgaacaatccggacctggtggc 594 qq

cacggacccgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaa 554 a Qγ

caayccgtcgtgccatgacgtgatcacggggctgtggactccgacggccagggatagcgc 773 caagcogtogtgcaacgcggtcgccaccggccagtggacgccctccgccgacgaccagcg 714 177 дq 0

agccggacgggtacccggggtatggtgtcatcaccaacgtcatcaacggcgggatccaatg 837 774 δy q

cggccatggcgaggacgatcgcatcgccgaccggatcggcttctacaagcgctactgcga 897 834 ŏ g

cattttcggcatcggctacgggaataacctcgactgctacaacca 957 q

894

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standard; cDNA; 1151 AAQ81346 AAQ81346

ВР

(first entry) 13-AUG-1995 AAQ81346;

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Rice chitinase RCH10 gene

Chitinase, RCH10 gene, transgenic plant, disease resistance, crop improvement, tobacco, Nicotiana tabacum, plant defense, crop improvement, tobacco, Nicotiana tu fungus pathogen, Cercospora nicotinae; Thanatephorus cucumeris; ss.

Oryza sativa

Location/Qualifiers 55..1065 /*tag= a

WO9502319-A

296

26-JAN-1995

15-JUL-1994;

93US-0093372. 16-JUL-1993;

356

STUDIES Maher EA, (SALK) SALK INST BIOLOGICAL Lamb CJ, Dixon RA,

WPI; 1995-067090/09 P-PSDB; AAR67969 associated pathogens when Transgenic plants contg. several plant defence proteins - have increased resistance to plant grown in crops as a food source

Disclosure; Page 31-32; 45pp; English.

The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) and an alfalfa beta-1,3-qlucanase coding sequence (AAQ81347) were incorporated into vectors for co-expression in transgenic tobacco, resulting in improved resistance to Cercospora nicotinae and Thanatephorus cucumeris fungal infection. BP

(first entry)

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Nucleotide sequence of a rice chitinase designated RCH10
           AAF54983 standard; DNA; 3035
                                                 15-MAY-2001
                               AAF54983;
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                                                               gttegggttetgeggeaccaceteegactactgeggeeeeegetgeeagageeagtgeac
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                                              27;
                            Length 1151;
                                               234; Indels
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Sequence 1151 BP; 197 A; 409 C; 353 G; 192 T; 0 other;
                            16;
                           Score 496.6; DB 1
Pred. No. 3.9e-78;
                                              0; Mismatches
                           51.18;
72.48;
                                              Conservative
                                     Similarity
                                    Local Simi
hes 684;
                            Query Match
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The present sequence encodes a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors comprise a heterologous extracellular domain (e.g. from a Bril protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xanthomonas spp. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to
Disease resistance protein; Xa21; RKK gene; transgenic plant; chitinase; Xanthomonas; plant pathogen; Bril protein; RCH10 protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgagcagtgcggctcgcaagccggcggcgccaagtgcgccgactgcctgtgctgcagcca 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    confer desired traits on essentially any plant.
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                                                                                                                                                                                                      "chitinase RCH10"
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pathogen control; disease resistance; molecular marker; ss.
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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB188995, and AAB18907-08 and AAB18900-01). The level of chitinases (AAB18895, AAB18897-98 and AAB18900-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful
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Matches 678; Conservative
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                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                   which
                                                                                        This sequence encodes Chitinase G. Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistant organisms. The genome of such transgenic organisms preferably contains more than one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so th
                                                                                                                                                                                                                                                                                                                                                                                                                    cactggctgcggtggcggcggcggcggggtggcctccatcgtgtccagggacctcttcga
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contg. at least 2 pathogen inhibiting genes genes with antifungal activity, show in disease resistance, also new DNA transfe
                                                                                                                                                                                                                                                                                          Length 1002;
                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                       the transgenic organisms have a greater degree of resistance resistance against a wider spectrum of diseases.
                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                             Sequence 1002 BP; 194 A; 329 C; 293 G; 186 T; 0 other;
                                                                                                                                                                                                                                                                                      Score 469.4; DB 15;
Pred. No. 2.1e-73;
); Mismatches 176;
                                                               Example 2; Page 13-14; 19pp; German
                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                      48.3%;
                                                                                                                                                                                                                                                                                                                 Conservative
Transgenic organisms - esp. plants contg. synergistic increase
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nes 575; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This cDNA encodes a floral organ-specific chitinase. The specification provides a promoter sequence (AAV49983) derived from rice associated with chitinase, specific to floral organs that allows expression of genes in the flower parts of monocotyledonous plants. The expression of desired genes specifically in the floral parts of monocotyledonous plants, allows modifications to be made in the structure or function of these parts allowing the introduction of desired characteristics such as increased resistance to bacterial attack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   caageeggeggegaagtgegeegactgeetgtgetgeageeagtteggggttetgegge 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         specific gene; chitinase; promoter; Oryza sativa; rice; monocotyledonous plant; bacterial resistance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Promoter sequence associated with chitinase, specific to floral organs - allows expression of genes in the flower parts of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1318;
                                                                                                                                                                                                                                                                                                                                                                             /product= "floral-organ specific chitinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        233; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1318 BP; 231 A; 442 C; 440 G; 205 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42.8%; Score 416.2; DB 11
Similarity 68.4%; Pred. No. 3.5e-64;
4; Conservative 0; Mismatches 233
                                                                                                                                                                                                            Floral organ-specific chitinase encoding cDNA
 taacctcgactgctacaaccaattgtcgttc 948
                             828 caacctcgattgctacagccagagacccttc 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takakura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Pages 33-35; 67pp; Japanese.
                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
114..1100
/*tag= a
                                                                                                                 BP.
                                                                                                            AAV49982 standard; cDNA; 1318
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                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (NISB ) JAPAN TOBACCO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monocotyledonous plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1998-388123/33.
P-PSDB; AAW64776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Inoue T, Ito T,
                                                                                                                                                                                                                                              Floral-organ
                                                                                                                                                                                                                                                                                                sativa
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                                                                                                                                                                               10-NOV-1998
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Matches 674
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                                                                                                                                                                                                                                                                                                                          879
                                                                                                                                                                                                                                                               2970 cttgactgctactctca 2986
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                                                                                                                                                                                                                                                                                                                                                                                              Chitinase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (NIHA ) JAPAN ENERGY CORP
                                                                                                                                                                                                                                                                                                                       AAT79940 standard; cDNA;
                                                                                                                                                                                                                                         922 ctcgactgctacaacca
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                                                                                                                                                                                                                                                                                                                                                                                        1. 40.8%; Score 396.2; DB 11; Length 4704; Similarity 67.2%; Pred. No. 9.6e-61; 76; Conservative 0; Mismatches 278; Indels 3;
                                                                                                                                                                                                            Recombinant DNA contg. high level promoter and plant chitinase gene - for transforming plants to over:express chitinase, imparting resistance to phytopathogenic fungi.
                                                                                                                                                                                                                                                                              Sequence encoding chitinase may be used to transform monoor dioctyledons to show increased resistance to fungal attack. A high level promoter is used from CMV 35s or 19s complement, NOS or OCS promoters of Agrobacterium opine synthetase gene, the RUBISCO small unit or the chlorophyl A/B binding protein.
                                                                                                                                                                                                                                                                                                                                                     Sequence 4704 BP; 1528 A; 783 C; 872 G; 1521 T; 0 other;
                                                                                                                             (DUPO ) DU PONT DE NEMOURS CO
                                                                                                       88US-0285252
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             /*tag=
                                                                                                                                                                          WPI; 1990-224529/29
                                                                                                                                                                                     P-PSDB; AAR05931
                                                                                                      16-DEC-1988;
                                                                                                                                                    BROGLIE KE,
                                  WO9007001-A
                                                         28-JUN-1990
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This sequence represents the coding sequence for the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi, plants have this enzyme to protect themselves from pathogenic fungi. Thus this enzyme can be used to prevent plants from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.
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                                                                                                                                      682 gogatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgacgtgatcacg
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us-09-534-229c-7.rng

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  879;
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  Length
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Score 375; DB 18;
Pred. No. 5e-57;
                        0; Mismatches
38.6%;
65.9%;
                       581; Conservative
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Query Match
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BP.

standard; cDNA;

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(first entry)

13-OCT-1997

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                                                                                                Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.
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(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER
                                Full length chitinase coding sequence
                                                                                                                                                                                                                                                                                                                                                                                    /product= chitinase
                                                                                                                                                                                                                                                                            Location/Qualifiers
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673 ttcaagacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgac 732
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al Similarity 64.4%;
572; Conservative (
              94US-0286020
                                    94US-0286020
                                                                                Sticklen MB;
                                                          (UNMS ) UNIV MICHIGAN
                                                                                                     1996-353879/35.
                                                                                                                 P-PSDB; AAW00186
            04-AUG-1994;
                                    04-AUG-1994;
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                      99c99g4g9cccaccgcgcccgacggcccttctcatggggctactgcttcaagcaggag
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                                                                                                                                                                                                                 361 ggagggtgggctacggcaccggatggcccatatgcgtggggatattgcttcataaggg--
                                                                cagggctcgccgagctactgcgaccagagcgccgactggccgtgcgcacccggcaag
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi; dutch elm disease; E. coli; chitinase-like protein; fungal infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              American elm chitinase-like protein coding sequence
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1153..1158
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This sequence represents the cDNA clone pHS2, which encodes a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHs0 used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gocacggocgagcagtgcggctcgcaagccggcggcgccaagtgcgccgactgcctgtgc 132
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   elm - u
plants
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1225 BP; 322 A; 277 C; 313 G; 313 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 370; DB 17; I
Pred. No. 3.6e-56;
0; Mismatches 310;
Isolated chitinase gene derived from an American obtain prods. for inhibiting fungal infection of
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ij

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916 caggiggiggatiggatiggatictacaagaggiacigigataticitagagitggctat 975
                                                                            tatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgac 852
                                                                                                                      aaggitggcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggctac 912
                                 gtgatcacggggctgtggactccgacggccagggatagcgcagccggacgggtacccggg
                                                                                       913 gggaataacctcgactgctacaaccaattgtcgttcaacgttgggctc
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AAX25613 standard; DNA; 7397 BP
                Banana ripening fruit Endo. DNA
            (first entry)
            02-AUG-1999
        AAX25613;
  AAX25613
RESULT
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fruit ripening; differential expression; fruit development; transgenic plant; ss

Musa acuminata.

W09915668-A2

01-APR-1999

23-SEP-1998;

97US-0060062 25-SEP-1997;

(BOYC-) BOYCE THOMPSON INST PLANT RES

Clendennen S, May G;

WPI; 1999-244425/20

P-PSDB; AAY05842, AAY05843, AAY05844

New isolated banana DNA molecules

Claim 5; Fig 16A-J; 143pp; English

This is the nucleotide sequence of a DNA molecule termed ENDO. The invention provides isolated DNA molecules which are differentially expressed during banama fruit development, and the protein products of these genes. The DNA is selected from a group comprising starch synthase, chitinase, endochitinase, beta-1,3-glucanase, thaumatin-like protein, ascorbate peroxidase, metallothionein, lectin and senescence-related protein. The regulatory elements of the genes can be used to produce chimeric genes for transformation of plants to provide controlled expression of heterologous DNA during fruit development, or in response to exogenous developmental signals, such as ethylene signals. The heterologous protein, e.g. therapeutic protein, can be isolated from the fruit or consumed directly in the transformed fruit. The identity of the present sequence is not given. The entire DNA sequence has been decoded in axevesance the amino acid sequences given in AAY05842-44.

Sequence 7397 BP; 2109 A; 1549 C; 1592 G; 2012 T; 135 other;

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5396 ggaggatgaaggeettgttgetggteatttttaeeettggeetegtegeteggegeetteg 5455
                                                                                                                                                    ccgagcaatgcggaaggcaagccgggggggctctctgccccgggggggtggtgtagcc 5515
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                                                                                                                       ccgagcagtgcggctcgcaagccggcggcgccaagtgcgccgactgcctgtgctgcagcc 139
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                                                                                                                                                                                 agttogggttotgoggcaccacctccgactactgoggccccgctgccagagccagtgca 199
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                                                         20 ggtgtgcgacggccgtcctggccgtcgtcgtgcggcggcggcggccggccacgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gccacggacccgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtcc
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                               90;
   Length 7397;
Score 337.6; DB 20; Length
Pred. No. 1.4e-50;
); Mismatches 302; Indels
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34.78;
61.58;
               Best Local Similarity 61.5
Matches 626; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 ctgcctcggcagaacaatgtggttcgcaggcgggaggtgcgcgttgtgcctcgggtctct 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcg 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was isolated from a N.tabacum cDNA library following screening with a partial tobacco intracellular chitinase clone. The gene can be inserted into an appropriate plasmid for production of transgenic plants having resistance to fungal pathogens. The sequence was modified so as to obtain apoplast targeting of the protein. G(961) was mutated to a T to create a STOP codon. A second STOP codon was created by mutation of T(968) to A and a Sall restriction site was created by changing T(975) to C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188 agagccagtgccctggtggtcccacaccccggtggtgggggatctcggcagtatcatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                getgeagecagttegggttetgeggeaceaecteegactactgeggeeeeege---tgee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 agagocagtgcactgg----ctgcggtggcggcggcggggggtggcctccatcgtgt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1152;
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                                                                                                                                                                                                                                                                                                       JS;
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JF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                           Plants with improved resistance to pathogenic fungi - chitinase and/or beta-1,3-glucanase genes modified for over-expression targetted to apoplasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other
                                                                                                                                                                                                                                                                                                      Van
Bol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 32.6%; Score 316.8; DB 12; Local Similarity 61.5%; Pred. No. 6.1e-47; Les 545; Conservative 0; Mismatches 332; :
                                                                                                                                                   10..984 /*tag= a /product= intracellular_chitinase
                                                                                                                                                                                                                                                                                                     Meulenhoff EJ, Woloshuk CP,
                                                                                  intracellular chitinase gene.
                                                                                                                                            Location/Qualifiers
                                                                                                    fungal resistance; phytopathogen;
                         ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 2; 55pp; English.
                                                                                                                                                                                                                                                                                                              Vloemans AA,
                                                                                                                                                                                                                                                                                                    Melchers LS,
                         DNA; 1152
                                                                                                                        Nicotiana tabacum Samsun NN
                                                                                                                                                                                                                                                                     (MOGE-) MOGEN INT NV.
(UYLE-) RIJKSUNIV TE LEIDEN
                                                                                                                                                                                                                                  91EP-0200191
                                                                                                                                                                                                                                                    90NL-0000222
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                1991-232019/32.
                      AAQ12898 standard;
                                                                                                                                                                                                                                                                                                              Sela-Buurlage MB,
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                                                                                                                                                                                                                                                                                                  Cornelissen BJ,
                                                                                                                                                                                                                                 30-JAN-1991;
                                                              14-OCT-1991
                                                                                                                                                                                                                                                    30-JAN-1990;
                                                                                                                                                                                                              07-AUG-1991
                                                                                                                                                                                           EP440304-A.
                                           AAQ12898
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               AAQ12898
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                                                                                                                                                                                                                                                                                                                                                                                                      607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cgigccaigacgigaicacgggggcigiggaciccgacggccagggaiagcgcagccggac 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         907
                                                                                                                                                                                                                                                                                                                                                               coggoaagcagtactatggccgcggccccatccagctcacccacaactacaactacggac 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaacaagccgt 721
482 agcaggagcagggctcgccgccgagctactgcgaccagagcgccgactgccgtgcgcac
                                                                                                                                                                                                                                                                                                      gggtacccgggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ggttctacacgtacgacgccttcttggccgccggcggcgttcccggccttcggcacca
                                                                                                                  ccggagacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacg
                                                                                                                                                                                                                                                                                                                                                                                                                                            cggcggccgcgaatcggggftggacctgctgaacaatccggacctggtggccacggacc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       848 gcactgactcaagggtccaggatcgcattgggttttacaggaggtattgcagtattcttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Intracellular chitinase; antifungal; transgenic plant; synergism;
beta-1,3-glucanase gene; tobacco; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             902 gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt 947
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10..78
/*tag= b
79..981
/*tag= c
/product= intracellular_chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nicotiana sp. intracellular chitinase cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; cDNA; 1152
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New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
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                             661
                                                                                                                              cagtaatctcattcaagtcagctctctggttttggatgactcctcaatcaccaaaacctt 727
                                                                                                                                                                781
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M, Van Roekel JSC;
                                                 ctggtcggaaatatttcggacgaggccccatccaaatttcacacaactacaggac
                                 cggcgggccgcgcaatcggggtggacctgctgaacaatccggacctggtggccacggacc
                                                                                                cgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaacaagacgt
                                                                                                                                                                 cgtgccatgacgtgatcacggggctgtggactccgacggccaggggtagcgcagccggac
                                                                                                                                                                                               728 cttgccacgatgtcatcattggaagatggcaaccatcgtctgctgaccgcgcagccaatc
                                                                                                                                                                                                                                 gggtacccgggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgg
                                                                                                                                                                                                                                                                788 gtctcoctggatttggtgtcatcacgaacatcatcaatggtggcttggaatgtggtcgtg
                                                                                                                                                                                                                                                                                                  ggcagaacgacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttcg
                                                                                                                                                                                                                                                                                                                   Chitinase; transgenic plant; beta-1,3-glucanase; antifungal;
plant resistance; pathogenic fungi; fungal resistant plant; ss.
                                                                                                                                                                                                                                                                                                                                                                   947
                                                                                                                                                                                                                                                                                                                                                                                    gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA sequence encoding an extracellular chitinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Socation/Qualifiers
10..984
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oshuk CP, Bol
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91US-0647831.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                 to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-qlucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fungi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1152;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
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                                                                                                                                                                Linthorst HJM, Melchers LS; 
ge MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 316.8; DB 18;
Pred. No. 6.1e-47;
0; Mismatches 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exhibit a synergistic antifungal effect.
                                                                                                                                                                              S, Sela-buurlage MB,
Woloshuk CP;
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llarity 61.5%;
Conservative
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                                                                               91US-0647831
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Best Local Similarity
Matches 545; Conserv
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                                             19-APR-1993;
                                                                               29-JAN-1991;
               23-SEP-1997
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The present sequence encodes an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic lungi. The recombinant polynucleotides and the process are useful for producing fungal resistant plants. 55555555**88**

2 71 cggccacggccgagcagtgcggctcgcaagccggcggcgacagtgcgccgactgcctgt 130 241 247 488 ttagagaacaatgtagccccggcgactactgtacaccaagtggtcagtggccttgtgctc 547 68 ctgcctcggcagaacaatgtggttcgcaggcgggaggtgcgcgttgtgcctcgggtctct 127 gotycagocagitogggitoigggcaccacotocgactactgcggcccccgc---tgcc 187 301 361 367 362 ccggagacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacg 421 427 422 agaccaccggcggtggcccaccgcgcccgacggcccttctcatggggctactgcttca 481 428 aaactacaggaggatgggcaacagcaccagatggtccatacgcgtggggttactgctggc 487 Gaps 188 agagecagtgeactgg-----ctgeggtggeggeggeggeggggggtggeetecategtgt 482 agcaggagcagggctcgccgagctactgcgaccagagcgccgactggccgtgcgcac 188 agagccagtgccctggtggtcccacaccacccggtggtggggatctcggcagtatcatct 242 ccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcg ggttctacacgtacgacgccttcttggccgccggcggcggttcccggccttcggcacca Length 1152; φ, .. Score 316.8; DB 21; Length Pred. No. 6.1e-47; 0; Mismatches 332; Indels Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other; 32.6%; 61.5%; Best Local Similarity 61.5 Matches 545; Conservative Query Match 131 302 ò g $\delta \lambda$ qq g qq qq QYg QΥ Ωp ŎΔ QQ QΥ δŽ δy

542 coggcaagcagtactatggccgcgggcccatccagctcacccacaactacagac 601

548 otggtcggaaatatttcggacgaggccccatccaaatttcacacaactacaactacggac

cggcggccgcgcaatcggggtggacctgctgaacaatccggacctggtggccacggacc 661

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842 ggcagaacgacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttcg 848 gcactgactcaagggtccaggatcgcattgggttttacaggaggtattgcagtattcttg

gggtacccgggtatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatgg

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gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt 947

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908 gigitagicciggigacaatcitgatigcggaaaccagaggictit 953

g

completed: May e: 7004 sec Search com

Appli Appli

Sequence Sequence

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Sequence 2, Application US/07704288C
Patent No. 5399660
GENERAL INFORMATION:
APPLICANT: LAMB. CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE GENES AND PLANT DEFENSE REGULATORY TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1151;
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STREET: 444 SOUTh Flower Street, Suite 2000
CITY: Los Angeles
STATE: California
COUNTRY: United States
Mermer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
SORTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 22-MAY-1991
CLASSIFICATION: 800
CLASSIFICATION: 800
NAME: Release Ketter, Stephen E.
REGISTRATION NUMBER: 31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51.1%; Score 496.6; DB 1;
llarity 72.4%; Pred. No. 1.9e-88;
Conservative 0; Mismatches 234;
US-08-971-217-7
US-09-350-600-7
US-08-047-413-8
US-08-047-413-8
US-08-081-213-8
US-08-181-253-8
US-08-449-315-12
US-08-449-315-12
US-08-449-043-12
US-08-455-265A-12
US-08-455-244-12
US-08-456-262-12
US-08-456-262-12
US-08-456-262-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
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INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: unknown
 COMPUTER READABLE FORM:
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Best Local Similarity
Matches 684; Conserv
 MEDIUM TYPE:
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/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PcTUS_COMB.seq:*
          GenCore version 4.5 (c) 1993 - 2000 Compugen Ltd.
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US-08-379-21

US-08-379-29-2

US-08-457-29-2

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US-08-1818-073A-9

US-08-1818-073A-9

US-08-286-020-1

US-08-286-020-1

US-08-477-413-1

US-08-477-413-1

US-08-401-56-1

US-08-401-56-1

US-08-401-56-1

US-08-448-03-7

US-08-448-03-7

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US-08-455-416-7

US-08-455-416-7
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Maximum Match 100%
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                                                        CAACCAGTGCGGCAGCCAGGCGGCGGCGGTGTGCCCCAACTGCCTCTGCTGCCAGCA
                                                                               gttegggttetgeggeaceacetecgaetaetgeggeeeeegetgeeagageeagtgeae
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Sequence 1, Application US/08093372 Patent No. 5530187 GENERAL INFORMATION: APPLICANT: Lamb, Christopher J. APPLICANT: Zhu, Qun

US-08-093-372-1

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APPLICANT: Maher, Eileen A.
APPLICANT: Maher, Richard A.
TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MULTIPLE TITLE OF INVENTION: DISEASE RESISTANCE GENES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 16-JUL-1993
CLASSIFICATION: 800
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COTHER INFORMATION: /product= "RICE CHITINASE"
US-08-093-372-1
                                                                                                                     ADDRESSEE: Pretty, Schroeder, Brueggemann & STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1151 base pairs
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                 COUNTRY: U.S.A. ZIP: 90071-2921
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NAME/KEY:
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US-08-379-259-2
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tcacgagaccaccggcgggtggcccaccgcggccggacggcccttctcatggggctactg
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                      477 CCACGAGACCACCGGCGGGGGGGGGGGGGCCCGACGGCCCCTACACGTGGGGCTACTG
                                                cttcaagcaggagca---gggctcgccgagctactgcgaccagaggcgccgactggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLANT DEFENSE GENES AND PLANT
DEFENSE REGULATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/379,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Reiter, Stephen B.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/704,288
FILING DAIE: 22-MAY-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE
TITLE OF INVENTION: DEFENSE
TITLE OF INVENTION: LEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08379259
Patent No. 5695939
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STATE: California
COUNTRY: United St
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                                                                                                                                                                                                                                                                                                                                                                    Score 496.6; DB 1;
Pred. No. 1.9e-88;
0; Mismatches 234;
                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 72.4%;
Matches 684; Conservative (
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                         TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                         CDS
55..1062
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Best Local Similarity
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us-09-534-229c-7.rni

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NAME/KEY:
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US-08-457-797A-9
                       OTHER : FEATURE:
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/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesi; and Fusarium sporotrichoides as
Well as Rhizoctonia solani and Botrytis cinerea."
LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
                                                                                                                                                                                                                                                                                           Transgenic pathogen-resistant organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
APPLICATION NOMBER: US/08/457,797A
FILING DATE: June 1, 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REGISTRATION NUMBER: 35,225
FEGISTRATION NUMBER: 35,225
                                                                                                                                894 cattttcggcatcggctacgggaataacctcgactgctacaacca 938
                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Transgenic pathogen-resistant or NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335 TELECOMMUNICATION: TELECOMMUNE (212) 408-2500
TELEFRONE: (212) 765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start= 64
                                                                                                                                                                                                                          Sequence 9, Application US/08457797A Patent No. 5689045 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (212,
TELEFAX: (212,
TELEFAX: 238555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TVPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
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905..910
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ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 1..63
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                       New York
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LOCATION:
                                                                                                                                                                                           RESULT 4
US-08-457-797A-9
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198 cactggctggcggtggcggcggcgggggggtggctccatcgtgtccagggacctcttcga 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                618 cggggtggacctgctgaacaatccggacctggtggccacggacccgacagtggcgttcaa 677
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OTHER INFORMATION: /note= "potential polyadenylation OTHER INFORMATION: signal"
                                                                                                                                           NAME/KEX: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                           /note= "probable signal peptide sequence"
                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence" FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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Pred. No. 3.5e-83;
0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48.3%;
76.6%;
                                                                                                                                                                                                             FEATURE:
NAME/KEY: sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 76.6
Matches 575; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: sig_peptide
LOCATION: 607..861
                                                    NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: sec
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LOCATION: 466..588
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133..861
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OTHER INFORMATION: /note= "p
OTHER INFORMATION: sequence"
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Matches 575; Conservative
                                                                                                                                                                                        NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: SEC
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LOCATION: 466..588
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133..861
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; LOCATION:
US-08-812-025-9
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/function="alf kD preprotein of chitinase G (ChiG)"
/product="antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                                                              857
738 cacggggctgtggactccgacggccagggatagcgcagccggacgggtacccgggtatgg 797
                                                                                                                 767
                                                                        798 tgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgacaaggt
                                                                                                                                                858 ggcggatcggatcgggttctacaagcgctattgtgacattttcggcatcggctacgggaa
                                                                                                                                                                      768 CGCCGATCGAATCGGGTTTTACAAGCGCTACTGTGACATCCTCGGCGTTGGCTACGGCAA
                                   648 CGCCGGCCAGTGGAGCCCGTCAGGGCTGACCGGGCCGCCAGGCCGGGTGCCCGGGTTTGG
                                                                                                 Transgenic pathogen-resistant organism 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,025
                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Transgenic pathogen-resistant or NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brunbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A29542 FWC - 37/31335
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Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
NAME: KOLG, Lisa
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 765-2519
TELERX: 238555
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDENS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
ORIGINAL SURCE:
ORGANISM: Hordeum vulgare
STRAIN: L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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OTHER INFORMATION:
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FEATURE:
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NAME/KEY: 5'UTR
LOCATION: 1..63
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U ZIP: 10112
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LOCATION:
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                                                                                                                                                                                                                                                                                                                       RESULT 5
US-08-812-025-9
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STATE:
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408 CTCCTCCGACTACTGCACCCCGAGGGCACATGGCCGTGCGCCCCGGGGAAGCGCTAACTA 467
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    318 egecttettggeegeegeeggeggegtteeeggeetteggeaceaceggagaeetggaeae 377
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                                           end not shown"
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                                                                          NAME/KEY: polyA_signal LOCATION: 905..910 OTHER INFORMATION: // note= "potential polyadenylation OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LCCATCON: 298..312
OTHER INFORMATION: _/note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LCGATCON: 349..379.
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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LOCATION: 607..861
OTHER INPORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "probable signal peptide
LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.3%; Score 469.4; DB 1;
76.6%; Pred. No. 3.5e-83;
live 0; Mismatches 176;
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588 GACGGCCATCTGGTTCTGGATGACGGCCGAGCCCAAGCCATCGAGCCATGCTGTGAT 647
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                                                                                                                                         648 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGCCGCAGGCCGGGTGCCCGGGTTTGG
                                                                                                                                                                           tgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgacaaggt
                                                                                                                                                                                              gacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgacgtgat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
TTGE OF INVENTION: Transgenic pathogen-resistant organism NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/138,873A
FILING DATE: AUGUST 24,1998
ATTOREX/AGRNT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
                                                                                                                                                                                                                                                                                                     918 taacctcgactgctacaaccaattgtcgttc 948
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Patent No. 6271438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Baker & Botts
30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Hordeum vulgare STRAIN: L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGIH: 1002 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64..861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New York
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-138-873A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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/codon_start= 64
/function= "chitinase"
/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/product= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 goggttoctgotcoatcgcaacgacgcagcgtgcctggcccgcgggttctacacgtacga 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 cactggctgcggtggcggcggcggggggggggcctccatcgtgtccagggacctcttcga 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 CGGATGCTTCTCCACGCAACGACGCCCTGCCAGGCCAAGGCTTCTACACCTACGA 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438 geceaecgegecegaeggecetteteatggggetaetgetteaageaggageagggete 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498 gccgccgagctactgcgaccagagcgccgactggccgtgcgcacccggcaagcagtacta 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  egecttettggeegeeggeggegetteeeggeetteggeaceaceggagaeetggaeac 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 1002;
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                                                                                                                                                                                                                                                                                                 CTHER INFORMATION: /note= "potential polyadenylation OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 298.312

CTHER INFORMATION: /note= "probable signal peptide

OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: sig_peptide
LOCATION: 349..378
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "probable signal peptide sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "probable signal peptide
                                                                                                                                                NAME/KEY: 3'UTR
LOCATION: 662..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 469.4; DB 4;
Pred. No. 3.5e-83;
0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sednence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 76.6%;
Matches 575; Conservative (
                                                                                                                                                                                                                                                            NAME/KEY: polyA_signal LOCATION: 905..910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: sig_peptide LOCATION: 298..312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /no
OTHER INFORMATION: seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig.peptide
LOCATION: 607..861
OTHER INFORMATION: /nc
OTHER INFORMATION: see
                                           INFORMATION:
                                                                INFORMATION:
INFORMATION:
                                                                                                         OTHER INFORMATION:
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; LOCATION;
US-09-138-873A-9
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0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 38.2%; Score 371.6; DB 1; Best Local Similarity 64.5%; Pred. No. 3.3e-64; Matches 573; Conservative 0; Mismatches 309;
                                                                                                                                                                                                                                                                                                                        LOCATION:
IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: DNA needed for chitinase
OTHER INFORMATION: in elm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: chitinase encoding DNA
                 MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Ulmus Americana
                                                                                                                                                                                                                                                                                                                                                                                          ; PUBLICATION INFORMATION: US-08-286-020-1
                                                                                                                                                     DEVELOPMENTAL STAGE: HAPLOTYPE: N/A
                                                                                                                     STRAIN: NPS 3-487 INDIVIDUAL ISOLATE:
                                                                                                                                                                                      TISSUE TYPE: N/A
CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: N/POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                        FEATURE
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408 CICCICCGACTACIGCACCCCGAGCGCACAATGGCCGTGCGCCCCCGGGAAGCGCTACTA 467
                               cacygggctgtggactccgacggccagggatagcgcagccggacgggtacccgggtatgg
                                                                                                                                                                                                                                                                                                      tgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgacaaggt
                                                                                                                                                                                                                                                                                                                                                                       ggoggatcggatcgggttctacaagogctattgtgacattttcggcatcggctacgggaa
                                                                                                                                                                                                                                                                                                                                                                                                     768 cecearceaarcecritiracaacecriaciereacarcereecerreecracecaa
                                                                                                   cggggtggacctgctgaacaatccggacctggtggccacggacccgacagtggcgttcaa
                                                                                                                                                                                                                                                                   648 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGGCCGCAGGCCGGGTGCCCGGGTTTGG
                                                                                                                                                                                                                                                                                                                                    708 TGTGATCACCAACATCAACGGCGGGATCGAGTGCGGTCACGGGCAGGACAGCCGCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08286020
Patent No. 5539095
GENERAL INFORMATION:
APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
TITLE OF INVENTION: A Chitinase cDNA Clone From a
TITLE OF INVENTION: Disease Resistant American
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                      918 taacctcgactgctacaaccaattgtcgttc 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                             828 CAACCICGAIIGCTACAGCCAGAGACCCIIC 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: MS-DOS 5.00
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/286,020
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4100
TELERA: (517) 347-4103
TELEX: No. 5539095e
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Nucleic Acid
STRANDEDNESS: Single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
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                                                                                                                       73 gecaeggeegageagtgeggetegeaageeggeggegeeaagtgegeegaetgeetgtge 132
                                                                                                                                                                                                                                          133 igcagccagitegggitetgeggeaceaecteegaetaetgeggeeeeegeigeeagage 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 433 gggtggcccaccggcccgacggccccttctcatggggctactgcttcaagcaggagcag 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GGCTGGGCAGGCAATGTGGAAGCCAAGCTGGGGGTGCAGTGTGTCCCGTTGGGCTCTGC 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggccgcggggttctacacg
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                                                                                                                                                                                                                                                                                193 cagigaciggetgeggiggeggeggeggeggggggiggeetecategtgiceagggaeete
                                                                                                                                                                                                                                                                                                                                                                                                                       262 CAATGIGGCGCCAGCGGTAGCGAIGAC----ATIGGCGGICTCATAICAAGCICCGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 316 TTTAATGACATGCTTAAGCATCGTAACGACGGTGGTTGTCCTGCCAAGGGGTTTTACACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 GGGTGGCAAGTGCACCCGACGGTCCATACTCTTGGGGATACTGCTACAATAGGGAGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 ggctcgccgccgagctactgcgaccagagcgccgactggccgtgcgcaccggcaagcag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                556 AACCCTTCCTTCCGATTATTGTTCTTTTAGTCCTACTTGGCCTTGTGCTTCCGGAAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     616 TACTITGGCCGTGGTCCCATTCAACTCCTGGAACTACAACTATGGACAGTGTGGAAGG
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Length 1225;
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Gaps

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tgcagccagttcgggttctgcggcaccacctccgactactgcggcccccgctgccagagc 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   316 TITAATGACATGCTTAAGCATCGTAACGACGGTGGTTGTCCTGCCAAGGGGTTTTACACC 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tacgacgcettettggscgccgccggcggtgttcccggcettcggcaccaccggagacetg 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gacacgcgggaagcgggaggtggcggccttcttcggccagacctctcacgagaccaccggc 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCACCGTAAAAAGGGAGATTGCTGCTTTCTTAGGTCAAACTTCCCATGAAACTACAGGT 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gggtggcccaccgcgcccgacggcccttctcatggggctactgcttcaagcaggagcag 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  556 AACCCTTCTTCCGATTATTCTTTTTAGTCCTACTTGGCCTTGTGCTTCCGGAAGAGA 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tactatggccgcggccccatccagctcacccaccactacaactacggaccgcgggccgc 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ttcaagacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgac 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgac 852
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                                                                                                                                                                                                                                                                                                                                                                                    TGCAGCAAATTTGGGTGGTGTGTGGGAGCACAAACGAGTACTGTGGTGATGGCTGCCAAAGC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cagigoaciggoiggoggoggoggoggoggoggoggoggoctocatogigiocagggacoic 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 CAATGIGGGGGGGGGGAAGCGAIGAC ----ATIGGGGGICTCATATCAAGCICCGCC 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 TATGATGCTTTTATTGCGGCTGCCAAGGCTTTCCCTGCATTTGGCTCCACCGGCGATGAT 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           616 TACTTTGGCCGTGGTCCCATTCAACTCTCCTGGAACTACAACTATGGACAGTGTGGAAGG 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcaatcggggtggacctgctgaacaatccggacctggtggccacggacccgacagtggcg 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 GCCATAGGAGCAAACCTATTAAACAACCCTGATCTCGTAGCAACTGACCCTGTCATTTCC 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               733 gigaicacggggcigigactccgacggccagggaiagcgcagccggacggacgggiacccggg 792
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64.5%; Pred. No. 3.3e-64;
live 0; Mismatches 309;
                                                                                                              NAME/KEY: chitinase encoding DNA
LOCATION:
IDENTIFICATION METHOD: sequencing
OTHER INFORMATION: DNA needed for chitinase
OTHER INFORMATION: in elm.
                                                                                                                                                                                                                                                                                                Best Local Similarity 64.5
Matches 573; Conservative
                                                                                                                                                                                                     ; PUBLICATION INFORMATION:
US-08-603-919-1
 CELL TYPE: N/A
CELL LINE: N/A
ORGANELLE: N/A
IMMEDIATE SOURCE: N/
POSITION IN GENOME:
FEATURE:
                                                                                                                                                                                                                                                                                 Query Match
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                                      gtgatcacggggctgtggactccgacggccagggatagcgcagccggacgggtacccggg 792
736 TICAAAACGGCCTTATGGTTCTGGATGACCCCAAGTCACAAAGCCCTCGTGCCATGAC 795
                                                                                                                               853 aaggtggoggatoggatogggttotacaagogctattgtgacattttoggcatoggctac
                                                                       tatggtgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggaacgac
                                                                                                                                                                                                                                                                               913 gggaataacctcgactgctacaaccaattgtcgttcaacgttgggctc 960
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela TITLE OF INVENTION: A Chitinase CDNA Clone From a TITLE OF INVENTION: Disease Resistant American TITLE OF INVENTION: Elm Tree COMMER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08603919
Patent No. 5728382
GENEZL INFORMATION:
APPLICANT: Masomeh B. Sticklen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: Acer
OPERATING SYSTEM: MS-DOS 5.00
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (517) 347-4100
TELEFAX: (517) 347-4103
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ATTORNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,9
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N/A
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN: NPS 3-487
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    US-08-603-919-1
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Recombinant gene coding for a protein having endochitinase activity or for a precursor thereof.
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    188 agagecagtgeactgg----ctgeggtggeggeggegggggtggectecategtgt
                                                                                          242 ccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcg
                                                                                                                    257 GATICTACAGTIACAAIGCCITTATCAAIGCTGCIAGGICTTTCCIGGCITIGGIACIA
                                                                                                                                                                                                                                                                      362 coggagacetggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacg
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STREET: King Street Station, Suite 500, 1800 Diagonal
STREET: Road, PO Box 299
CITY: ALEXANDRIA
STATE: VIRGINIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/07842165
Patent No. 5932698
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APPLICANT: DUBOIS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGUAY, Jean Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
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                                                                                                                                                                                                                                                                                                    APPLICANT: LEGGAX, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                     gggaataacctcgactgctacaaccaattgtcgttcaacgttgggctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NOMBER: US/08/475,427
FILING DAWE: 07-7UN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DAWE: 01-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FF91/00607
FILING DATE: 21-7UL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 16781/564/BEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DAIA:
APPLICATION UNMBER: FR 90 09460
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     US-08-475-427-15
Sequence 15, Application US/08475427
Patent No. 5859340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PELECOMMUNICATION INFORMATION
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                                                                                                                                                                                                                                                                      Michel
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                      DUBOIS,
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nes 546; Conserv
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: DUBOIS
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-047-413-10
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGCCAGTGCCCTGGTGGTCCCACACCACCGGTGGTGGGGGATCTCGGCAGTATCATCT 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 GIGGIGATACCACIGCCCGIAAAAGAGAAAICGCGGCITICTICGCCCAAACCICCCAIG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  437 TTAGRGAACAAGGTAGCCCCGGCGACTACTGTACACCAAGTGGTCAGTGGCCTTGTGCTC 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cgacagtggcgttcaagacggcgatatggttctggatgacgacgcagtccaacaagccqt 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 agagccagtgcactgg-----ctgcggtggcggcggcggcgggggtggctccatcgtgt
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                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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les 331;
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                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/348
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                APPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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ilarity 61.6%;
Conservative C
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TELEFAX: (703) 683-4109
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
COMPUTER READABLE FORM:
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Best Local Similarity
Matches 546; Conserv
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APPLICANT: BOJ, JOHN F.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: DETAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
cgtgccatgacgtgatcacggggctgtggactccgacggccagggatagcgcagccggac
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Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
Sela-Buurlage, Marianne B.
Vloemans, Alexandra A.
Woloshuk, Charles P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cornelissen, Bernardus J.C.
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19-APR-1993
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APPLICATION NUMBER: US 07/647,831
FTLING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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:: 755 Page Mill Road
Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 10, Application US/08047413
Patent No. 5670706
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REFERENCE/DOCKET UNBABER: 24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ADDRESSEE: Morrison &
STREET: 755 Page Mill
CITY: Palo Alto
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GENERAL INFORMATION:
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                                                                                                                       71 eggecaeggecgageagtgeggetcgeaageeggegegegecaagtgegeegaetgeetgt 130
                                                                                                                                                     68 CTGCCTCGGCAGAACAAIGTGGTTCGCAGGCGGGAGGTGCGCGTTGTGCCCTCGGGTCTCT 127
                                                                                                                                                                                   gotgeagecagitegggitetgeggeaceaecteegaetaetgeggeeeege---tgee 187
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                                                                                                                                                                                                                                                                                                           242 ccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggcccgcg
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6
                                                             Length 1152;
                                                        Score 316.8; DB 1; Length
Pred. No. 1.4e-53;
0; Mismatches 332; Indels
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Best Local Similarity 61.5%;
Matches 545; Conservative
 10..981
; LOCATION:
US-08-047-413-10
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Sequence 10, Application US/08229050 Patent No. 6066491

RESULT 12 US-08-229-050-10

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                 APPLICANT: Melchers, Leo S.
APPLICANT: Melchers, Leo S.
APPLICANT: Wendenhoff, Elisabeth J.S.
APPLICANT: Wan Rockel, Jeroen S.C.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Vloemans, Alexandra A.
APPLICANT: Woloshuk, Charles P.
APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT TITLE OF INVENTION: DOLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
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COMPUTER READABLE FORM:
COMPUTER: READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,050
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 316.8; DB 3;
Pred. No. 1.4e-53;
0; Mismatches 332;
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ATTORNEY/AGENT INFORMATION:
NAME: MATESTAGE, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-20022.00
TELEPHONE: 415-494-0792
TELEPHONE: 415-494-0792
Cornelissen, Bernardus J.C.
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APPLICATION NUMBER: US 07/647,831
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61.5%;
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LENGTH: 1152 base pairs
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Best Local Similarity 61.5'
Matches 545; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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STATE: California
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US-08-229-050-10
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TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
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                                                                                               agaccaccggcgggtggcccaccgcgcccgacggccccttctcatggggctactgcttca 481
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ggttctacacgtacgacgccttcttggccgccggcgcgttcccggccttcggcacaa
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Patent No. 6087560
GENERAL INFORMATION:
APPLICANT: Cornelissen, Bernardus J.C. APPLICANT: Melchers, Leo S. APPLICANT: Melchers, Leo S. APPLICANT: Wan Rockel, Jeroen S.C. APPLICANT: Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vloemans, Alexandra A. APPLICANT: Woloshuk, Charles P. APPLICANT: Bol, John F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEE: Morrison & Foerster: 755 Page Mill Road
Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
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US-08-801-563-10
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APPLICANT:
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SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                            FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-AN-1991
ATORNEY/AGENT INFORMATION:
NAME: MILESPACE 29,959
REGISTRATION NUMBER: 29,959
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-494-0792
                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/047,413
                                                                   US/08/801,563
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61.5%;
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INFORMATION FOR SEQ ID NO:
                                              CURRENT APPLICATION DATA
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                                                                 APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 800
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Best Local Similarity
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US-08-801-563-10
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DNA (genomic)
                                                            27.18;
                                                                             Best_Local Similarity 59.99
Matches 505; Conservative
 ) MOLECULE TYPE:
US-08-475-427-14
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US-07-842-165-14
                                                              Query Match
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APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
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 508 CTIGIGGAAGAGCCATAGGAGIGGACCICCIAAACAAICCIGAITTAGIGGCCACAGAIC 667
                                662 cgacagtggcgttcaagacggcgatatggttctggatgacgacgccgtccaacaagccgt
                                                                                                                           728 CTTGCCACGATGTCATGGAAGATGGCAACCATCGTCTGCTGACGCGCGCAGCCAATC
                                                                                                                                                                                                                                                     848 GCACTGACTCAAGGGTCCAGGATCGCATTGGGTTTTACAGGAGGTATTGCAGTATTCTTG
                                                                                               ogtgccatgacgtgatcacggggctgtggactccgacggccaggggtaggcgcagccggac
                                                   gggtacccggggtatggtgtcatcaccaacgtcatcaacggcgggggtatccaatgcggcatgg
                                                                                                                                                                                          788 GTCTCCCTGGATTTGGTGTCATCACGAACATCATCAATGGTGGCTTTGGAATGTGGTCGTG
                                                                                                                                                                                                                         842 ggcagaacgacaaggtggcggatcggatcgggttctacaagcgctattgtgacattttcg
                                                                                                                                                                                                                                                                                      902 gcatcggctacgggaataacctcgactgctacaaccaattgtcgtt 947
                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 16781/564/BEDL
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEE: Foley & Lardner
: 3000 K Street, N.W., Suite 500
Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/842,165
FILING DATE: 01.AMYT1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21.JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/475,427 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 14, Application US/08475427
Patent No. 5859340
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
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TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Foley & L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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TOPOLOGY: lin
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US-08-475-427-14
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                                                  Gaps
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Length 905;
  Score 263.8; DB 2;
Pred. No. 2.6e-43;
0; Mismatches 317;
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NERAL INFORMATION.
NICHEL
APPLICANT: DUBOUS, Michel
APPLICANT: GRISON, Rene
APPLICANT: LEGGAY, Jean-Jacques
APPLICANT: LEGGAY, Jean-Jacques
APPLICANT: TOPPAN, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
""""" SEQUENCES: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 905;
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                                                                                                                                                       ADDRESSEE: FOLEY & LARDNER
STREET: King Street Station, Suite 500,1800 Diagonal
STREET: Road, PO Box 299
                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FAPLICATION NUMBER: US/07/842,165
FILING DATE: 19920501
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 263.8; DB 2;
Pred. No. 2.6e-43;
0; Mismatches 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    16781/348
                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
ATTORNEY-AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REPERFORC/POCKET NUMBER: 1678:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELER: 000140
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Best Local Similarity 59.9%;
Matches 505; Conservative C
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TELEN: 99149
INFORMATION FOR SEQ ID NO: 14
SEQUENCE CHARACTERISTICS:
LENGTH: 905 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                 Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: single
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                   ALEXANDRIA
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PY: USA
22313-0299
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 GENERAL INFORMATION:
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Search completed: May 3, 2002, 16:27:02 Job time: 7296 sec

HVSME1002

HVSMEK000 WHE0965_F HVSMEa001

Sc02_08b0 HVSMEK000 HVSMEh009 HVSMEh009 HVSMEh008 ISC003.D0 HVSME1002

HVSME1000 HVSMEh009 HVSME1000

HVSME1001

WHE313_F0 HVSME1000 WHE0327_A HVSME1001

HVSMED001

HVSMEh009

HVSMEC001

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on:

Sequence:

Title:

Searched:

Database

178459788787 1784597887

Result No.

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HV_CED0022E17f Hordeum vulgare seedling green leaf EST 11brary HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone HV_CED0022E17f, mENA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Triticeae; Hordeum.

1 (bases 1 to 816)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, X., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                BG313150 WHE2054 D
BG416746 HVSMEK001
                                                                                                                                                                                                                                                          BG366294 HVSME1000
BG907369 Talr1159E
BE602137 HVSMEh010
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BE405888 WHE0401_d
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                BE425245 WHE313_A0
BG365634 HVSME1000
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BG425368 W
BG365157 H
BB426069 W
BG367616 H
BG301220 H
                                                                                                                                                                                  BG365326 BF620099 BE454845 B
                                                                               BG368854
BE705117
BE6415203
BE6455203
BE6454366
BG366386
BE455238
BE655238
BE611224
BG36588 B
                                          BG416746
BG414551
BE498719
BF624146
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Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 792.
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BE455238
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BG367460
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BG366294
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Hordeum vulgare
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BE455567 HYSME1000
BF61746 HVSME1000
BF61746 HVSME1000
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3395.224 Million cell updates/sec
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                                                                3, 2002, 16:23:53 ; Search time 3076.35 Seconds
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          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                     11351937 seqs, 5372889281 residues
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363 eggagaeettggaeaegeggaagegggaggtggeggeettetteggeeagaeeteteaega 422
 ACCEGIACCCGGATACCGCGIGATCACCAAC
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ilarity 92.8%;
Conservative 0
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                                                                          /lab_bost="SolR"

/lab_bost="Yector: lambdaZAP: Site_1: EcoR1; Site_2: Xhol: For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/Darley/ To order a clone see http://www.genome.clemson.edu/orders"

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                         /clone="HV_CEb0022E17f"
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1.1e-116;
les 71; I
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Pred. No. 2.1e-
0; Mismatches
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
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91.1%;
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Sequence trimming: Vector sequences and sequence ends were trimmed from the 5'-and 3'-end until a 50 bp window contains less than two ambiguities. The maximum length was set to 700 bp."

233 c 98 t 1 others
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1; Poales; Poaceae; Pooideae
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Michalek, W., Weschke, W., Pleissner, K.-P. and Graner, A.

BST sequencing and analysis in barley
Unpublished (2000)
Contact: Michalek W

Institute for Plant Genetics and Crop Plant Research
Corrensstr. 3, D-06466 Gatersleben, Germany
Email: michalek eigher gatersleben, dermany
Email: michalek eigher gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: Mi3rev primer for 3'end.

Location/Qualifiers
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/lab_host="XLIBlue"
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Spermatophyta, Magnoliophyta, Liliopsida;
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Pred. No. 1.4e-94;
0; Mismatches 46
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816
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/db_xref="taxon:4513"
/clone="HK01K20r"
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://pgrc.ipk-gatersleben.de
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/clone_lib="Hordeum vulgare Barke etiolated leaves"
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                                          gaccaccggcgggtggcccaccgccgacggccccttctcatggggctactgcttcaa
                                                                                                                                                                                                                                                                           gacagtggcgttcaagac~ggcgatatggttctggatgacgacgcagtccaa 713
                                                                                                                                                                                                                                                                                           Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute for Plant Genetics and Crop Plant Research Corrensstr 3, D-06466 Gatersleben, Germany Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gSeq primer: Ml3rev primer for 3'end.
Location/Qualifiers
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/lab_host="XLIBlue"
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/cultivar="Barke"
/db_xref="taxon:4513"
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AL500402.1 GI:12026638
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Gaps

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Length 693;

DB 10;

Score 533.6; DB 10 Pred. No. 1.4e-88; 0; Mismatches 51,

Match 54.9%; Local Similarity 91.6%; Les 597; Conservative

Query Match Best Local S: Matches 597,

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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 616)
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Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Tong,J.C.
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Email: oandersn@pw.usda.gov
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Anderson, O.D., Chac
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                                                                                                                                                                                                                                                                                                                                                         egactgcctgtgctgcagccagttcggggttctgcggcaccacctccgactactgcggccc 179
                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                               Length 616;
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sequence with phred score less than 20
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                                                                                                                                                                                                                                                                                                               Score 520.2;
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            Seq primer: Strategene SK primer.
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                       Location/Qualifiers
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211 c 19
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91.2%;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae; Triticaea; Triticum.

1 (bases 1 to 508)

S Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Fenillet,C., Gale,M., Graner,A., Gustufson,P., Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudlier,P., Eangridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Oqihara,Y., Pecchioni,N., Qualset,C., Schuch,M., Salvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
International Triticeae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3
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yta; Liliopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Canada
                                                                                             BE430003 508 bp mRNA EST 26-JUL-2000 TASO06.A08R990616 ITEC TAS Wheat CDNA Library Triticum aestivum DB430003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant Biotechnology Institute, National Research Council of 110 Gymnasium Place, Saskatoon, SK S7N 0W9 Canada Tel: 306 975 5577 Fax: 306 975 4839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccagagccagtgcactggctgcggtggcggcggcggcggggggtggcctccatcgtgtccag
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188 c 175 g 79 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: Gopalan.Selvaraj@nrc.ca
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.5%; Score 471.6; DB 10;
llarity 97.8%; Pred. No. 3.2e-77;
Conservative 0; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .508
/organism="Triticum aestivum"
/db_xref="taxon:4565"
/clone="TAS006.A08"
                                                                                                                                                                                                                                  BE430003.1 GI:9427846
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GTCATGCCATGACGTGA
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hes 499; Conserv
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ggaagogggaggtggcottcttcggccagacctctcacgagaccaccggcgggtggc 439
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                                                                                                                                                                                                            440 ccaccgcgcccgacggccccttctcatggggctactgcttcaagcaggagcagggctcgc 499
                                                                                                                                                                                                                                                                                                                                      241 CACCGAGCTACTGCGACCAGAGCGCCGACTGGCCGTGCGCACCCGGCAAGCAGTACTATG 300
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BG365536
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/tissue_type="Spike before anthesis"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZaP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhOI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly/A) RNA were prepared, a CDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors).

83 a 174 c 151 g 71 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                    BGZ65207 480 bp mRNA EST 16-FEB-2001 WHE2339_C11_F21ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2339_C11_F21, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 480)
Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han P.S., Hais, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
    485
                                                                                                              421 CACCGGGGGGGGG-CCACCGCGCCCGACCTTTCT-ATGGGGCTACTGCTTCAAACA 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.

Location/Qualifiers
                                                                                          caccggcgggtggcccaccggcgcccgacggccccttctcatggggctactgcttcaagca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .480
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE2339_C11_F21"
                                                                                                                                                                                                   ggagcagggctcgccgccgagctactgcga 515
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                                                                                                                                                                                                                                                                                                                                                                                                                BG263207.1 GI:12865133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                           bread wheat
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AUTHORS
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KEYWORDS
SOURCE
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BG263207
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/tissue_type="20 DAP spike"
/lab_host="SolR"
/note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: Xhol; For more details on library preparation and sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yv., Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, Y., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                    BG36536 805 bp mRNA EST 08-MAR-2001
HVSME10003B22f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare CDNA clone HVSME10003B22f, mRNA sequence.
BG365536
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eggegatatggttetggatgaegaegeagteeaacaageegtegtgeeatgaegtgatea 739
                                                                                                       EST library
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/clone_lib="Hordeum vulgare 20
HVcDNA0010 (20 DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clemson University Genomics Institute
Clemson University
100 Oordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 778.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                          BG365536.1 GI:13254635
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Unpublished (2000)
Contact: Wing RA
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Pred. No. 2.9e-74;
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
1 (bases 1 to 584)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST library
                                                                                         Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                     Development of a genetically and physically anchored EST resource
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Unpublished (2000)
On Jul 26, 2000 this sequence version replaced gi:9465371.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7228
Fax: 864 656 4293
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anther)"
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88.0%; Pred. No. 5.1e-74;
Live 0; Mismatches 68; Indels 1;
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/db_xref="taxon:4513"
/clone="HYSMEG0017N15f"
/clone="HYSMEG0017N15f"
/clone=Lib="Hordeum vulgare pre-ant!
HVCDNA0008 (white to yellow anther)
/tissue_Lype="pre-anthesis spike"
/lab_host="SOLR"
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Seq primer: AATTAACCCTACTAAGGG
High quality sequence stop: 567.
Location/Qualifiers
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1 (bases 1 to 935)
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                                                                                                                                                                                                                                                                                                                                                                                          "Vomeluuvaluyi Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare CDNA clone HVSME10004109f, mRNA sequence. BG365857
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Unpublished (2000)
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                                                                                                                    aagcaggagcagggctcgccgccgagctactgcga-ccagagcgccgactggccgtgcgc
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Pred. No. 2.3e-69;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Hordeum vulgare 20
HycDMNO10 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SoLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 Jordan Hall, Člemson, SC 29634, USA
Tel: 864 656 7288
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Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                            GCCCAGCAAGCAGTGCTTTGGCCCGGGCCCCATCC 583
                                                                                                                                                                                              540 acceggeaageagtactatggeegeggeeceatee 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEi0004109f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 626.
Location/Oualifiers
                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 617)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Ming, R., Close, T.J., Kleinhofs, A., Wise, R., Benmer, M., Rambo, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
Development of a genetically and physically anchored EST resource for barley genomics
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                                                                                                                                                                                                                                                                   caccacoggagacetggacacgcggaagcgggaggtggcggccttcttcggccagacete 416
                                                                                                                                                                                                                                                                                                     teaegagaecaceggegggtggeceaecgegecegaeggeecetteteatggggetaetg 476
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CGGCGGCGGCAGCACGCCCGTCACGCCCATCGGGCGGCGGCGGCGTGTCCTCCAT 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 22-FEB-2001
shoot EST library
                                                        cgtgtccagggacctcttcgagcggttcctgctccatcgcaacgacgcagcgtgcctggc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cggaccggcggccgcgaatcggggtggacctgctgaacaatccggacctggtggccac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                759 AGCCGTCGAGGCCTTCCTGTGATCACCGGCCAATGGGACCCCTTAAGAACAGGACCGGGC
                                                                                                                                                                   ccgcgggttctacacgtacgacgccttcttggccgccgccggcgttcccggccttcgg
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HYCDNA0003 (Etiolated and unstressed) Hordeum
HYSNEc0009B09f, mRNA sequence.
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617

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ggcgggccgcgaat
                            GATAGGGCGGTCAAT
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Wood,T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               3,
                                                                                                                                                                                                                                          /clone_lib="Hordeum vulgare seedling shoot EST library HVCDNA0003 (Friolated and unstressed)" /tissue_type="Seedling shoot" /lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ccacgetgagagegeggtgtgegaeggeegteetggeegtegteetggeggeggeegg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   244 GCGACCTCTTCGAGCGGTTCCTCCTCCATCGCAACGACGCGGAGTGCCTGGGCCCCGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gagacctggacacgcggaagcgggaggtggcggccttcttcggccagacctctcacgaga
              On Dec 18, 2000 this sequence version replaced gi:11883480.
Contact: Wing RA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 422.4; DB 11;
Pred. No. 3.5e-68;
0; Mismatches 97;
                                                                        Člemson, SC 29634, USA
                                           Clemson University Genomics Institute
Clemson University
                                                                                                                                                                             1. .617
/organism="Hordeum vulgare"
                                                                   100 Jordan Hall, Clemson, SC 29034,
Tel: 864 656 4298
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCTCACTAAAGGG
High quality sequence stop: 541.
                                                                                                                                                                                                        /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEc0009B09f"
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Best Local Similarity 83.6%;
Matches 514; Conservative
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Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta; Triticeae; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum; 1 (bases I to 729)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVCDNA0009 (5 to 45 DAP)"

Tissue_type="5-45 DAP Spike"

/lab_nost="SoL#" SoL#"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
BE602672 729 bp mRNA EST 02-MAR-2001
HVSNEh0101A21f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSNEh0101A21f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 239 c 110 t l others
                                                                                                                                                                                                                                                                                                                                                                              Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 CATGGCCATCGGCACGCGCGCGCGGCAGCGTCCTCCATCATCTCGCGCGCACACATTCGA 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         258 geggtteetgeteeategeaacgaegeagegtgeetggeeegegggttetaeaegtaega
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Hordeum vulgare"/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SC 29634,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson,
                                                                                                                     BE602672
BE602672.1 GI:9860233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for barley genomics
Unpublished (2000)
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
                                                                                            mRNA sequence.
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Indels
/tissue_type="Etiolated shoot"
/dev_stage="Five day old seedling"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 413.8; DB 10;
Pred. No. 1.3e-66;
0; Mismatches 42;
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91.3%;
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Best Local Similarity
Matches 439; Conserv
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KEYWORDS
SOURCE
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Triticeae; Triticum.

[ (bases 1 to 482)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Normalized shoot cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE488961 482 bp mRNA EST 31-JUL-2000 WHE1077_C01_F01ZS Wheat unstressed seedling shoot normalized cDNA library Triticum aestivum cDNA clone WHE1077_C01_F01, mRNA
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/clone_lib="Wheat unstressed seedling shoot normalized
cDNA library"
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                                                                                                                                                                                                                                                              677
                                                                                                                                                                                                                                                                                                                                           gacggcgatatggttctggatgacgacgcagtccaacaagccgtcgtgccatgacgtgat 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     798 tgtcatcaccaacgtcatcaacggcgggatccaatgcggcatggggcagaacgacaaggt 857
                                                               276 GGCGACGGCACCGGACGGGGCCTTCGCCTGGGGCTACTGCTTCAAGCAGGAACGCGGCGC 335
                                                                                                      557
                                                                                                                                           336 CTCCTCCGACTACTGCACCCCGAGCGCACAGTGGCCGTGCGCCCCCGGGAAGCGCTACTA 395
                                                                                                                                                                                  617
                          goccaccgcgcccgacggccccttctcatggggctactgcttcaagcaggagcaggggctc 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                   eggggtggacctgctgaacaatccggacctggtggccacggacccgacagtggcgttcaa
                                                                                                                                                                                                                                                                                     738 cacgggggttgtggactccgacggccagggatagcgcagccggacgggtacccgggtatgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           558 tggccgcggccccatccagctcacccaccaactacaactacggaccgggggccgcgcaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                576 CGCCGGCCAGTGGAGCCCGTCAGGGGCTGACCGGGGCCGCAGGCGGGTGCCCGGGTTTGG
                                                                                                        498 geogeegagetaetgegaecagagegeegaetggeegtgegeaeeeggeaageagtaeta
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          696 CGCCGATCGAATC-GGITITACAAGCGCIACIGIG 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ggcggatcggatcgggttctacaagcgctattgtg
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Fax: 5105595818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence.
BE488961
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                            438
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BE488961
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KEYWORDS
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/note="Vector: Landad Uni-ZAP XR, excised phagemid phluescript SK; Site_1: BcoRL; Site_2: Xhol; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of callifornia, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares'. Plasmid DNA protocol.
                                                                                                                                                                                                                                                                                                                                                          HT Nguyen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG368852 623 bp mRNA EST 08-MAR-2001
HVSWE10020P03f Hordeum vulgare 20 DAP spike EST library HVcDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSWE10020P03f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                               preparations and DNA sequencing were performed in the Anderson lab (all other authors)." 170~c~161~g~83~t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           422 GCCACCGCACCGACGGCCCCTTCTCATGGGGCTACTGCTTCAAGCAGAGAAGAGTCCG 481
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae, Triticeae, Hordeum.
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1 (bases 1 to 93)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
Wing, R., Close, T.J., Kleinhofs, A., Kernodle, S., Palmer, M., Rambo
, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVSME10004K07f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10004K07f, mRNA sequence. BG365887.1 GI:13254986
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                                                                                                                                                                    gtgcggctcgcaagcoggcggcgccaagtgcgccgactgcctgtgctgcagccagttcgg 146
  GGTGGCCACGGACCCGACCGTGTCGTTTAAGACTGCGATGTGGTTTTGGATGACGGCCCA 480
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HycDNN0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SolR"
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                                                     708 gtccaacaagccgtcgtgccatgacgtgatcacgggggctgtggactccgacggccaggga
                                                                                                           27 gacggccgtcctggccgtcgtcctggcggcggcgggggcgcggccggccgggcgggca
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: AATTAACCOTCACTAAAGGG
High quality sequence stop: 888.
Location/Qualifiers
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/clone="HVSMEi0004K07f"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: rwing@clemson.edu
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                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Mainta, Main
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see http://www.genome.clemson.edu/projects/barley/ To
order a clone see http://www.genome.clemson.edu/orders"
1 225 c 198 g 94 t l others
                                                                                                                                                                                                                                            Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
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Pred. No. 9e-65;
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HycDMx0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SolR"
                                                                                                                                                                                                                                                                                                                                                                                            Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 728
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA Clemson University Genomics Institute
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
/clone="HVSME10020p03f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
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Location/Qualifiers
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78.4%;
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RESULT 1 BE425245

LOCUS

ACCESSION VERSION KEYWORDS REFERENCE

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/clone="WHEB13_A05_A05"
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/dev_stage="Five day old seedling"
/dev_stage="Five d
        Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
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                                                                                                                                                                                                       Email: oandersneepw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
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/cultivar="Chinese Spring"
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae;
'Triticeae; Triticum.'
1 (bases 1 to 498)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
.P.S., Hsla,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.L. and Iong,J.C.
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Search completed: May 3, 2002, 16:24:10 Job time: 7210 sec

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Query
Result
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SUMMARIES

script	X76041 T.aestivum AF280437 Secale ce AF000955 Poa prate AF000966 Poa prate AF000964 Poa prate D16223 Rice Cht-3 AP003685 Oriza sat	rdeum Secal Ccacca Ccacca Setiv Sativ Sativ Sativ Sativ Sativ	A37990 Sequence 9 A8703754 Sequence 9 175200 Sequence 9 134210 Hordeum vul 100073 Zea mays ac Z2962 C.sativa (P D16222 Rice Cht-2 AB012855 Coryza sat Z78202 Persea amer Z78202 Persea amer Z78202 Persea amer Z78202 Persea amer Z78202 Persea mays Cl M94105 Allium sati X15349 Barley (H.v M13966 Pv vulgaris A8015655 Cucutobita S4326 CH5B=Chitin X1633 NGCOtiana t A8048531 Psophocar M94106 Allium sati E13290 CDNA encodi	ndochitinas hryophyta; Poales; Poa
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GSTSDYCGNCCQSQCNGCSGGGTPVPVPTPTGGGGVSSIISOSLFDQMLLHRNDAACQA
KGFYNYGAFVAAANSFSGFATTGGADVPKREVAAFLAQTSHETTGGMPTAPDGPFSWG
YCFNOERGAASDYCSPNSQMPCAAPGKKYFGRGPIQISYNYN'CFAGRAIGTDLINNYD
LVATDATVSFKTALMFWMTPQSPKPSSHDVITGRWSPSGADQAAGRVPGYGVITNIIN
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in isogenic lines by infection with Puccinia graminis i. 103, 177-187 (1994)
Location/Qualifiers
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                                         1. .1985
/organism="Triticum aestivum"
/cultiar="Chinese spring"
/db_xref="taxon:4565"
/clone_lib="lambda gem-12 genomic"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 875; DB 8; 1
Pred. No. 3.5e-116;
); Mismatches 45;
                                                                                                                                                                                                                                                                                                                                            /db_xref="SPTREMBL:Q41539"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="endochitinase"
554 c 552 g 41.
                                                                                                                                                                                                                                                                                                     /product="endochitinase"
/protein_id="CAA53626.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91.1%;
llarity 95.0%;
Conservative 0
                                                                                                                       /1. .75
/gene="CHI"
250.
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/gene="CHI"
693. ,1
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/gene="CHI"
529. .536
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/gene="CHI"
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71. .75
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600. .>1595
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/gene="CHI"
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Matches 915; Conser
  induced in
Plant Sci.
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Eukaryota, Viridiplantae, Embryophyta, Tracheophyta, Spermatophyta,
Magnoliophyta; Liliopsida, Poales, Poaceae, Pooideae, Triticeae;
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                                   1053 ACCTCCCACGAGACCACCGGGGGGGGGCCAACGGGCCCCCAACGGCCCCCAACGGCCCCTACTGGGGC
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                                                                                               tactgetteaaceaggagegegegeeecteegactactgeaegeegagetegeagtgg
                                                                                                                                                                                           ccatgtgcgccgggcaagaagtacttcgggcgcgggcccatccagatctcacacaactac
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Submitted (20-JUN-2000) Biology, University of Waterloo,
University Ave West, Waterloo, ON N2L 3G1, Canada
Location/Qualifiers
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Yeh,S., Moffatt,B., Griffith,M., Xiong,F., Yang,D.S.C.,
Wiseman,S.B., Sarhan,F., Danyluk,J., Xue,Y.Q., Hew,C.L.,
Doherty-Kiby,A. and Lajoie,G.
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/variety="Musketeer"
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Tracheophyta;
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766 AAACCTTCGAGCCACGACGTGATCACGGGCCGGTGGAGCCCCTCGGGCGCGCGAGGCA 825
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                               1 atgagaggagttgtggtggtggtggccatgctggccgcggccttcgccgtgtctgcgcacgcc
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                                                                                             gggcgcgggcaggacggccgtgtcgccgaccggatcgggttctacaagcgctactgcgac
                                                                                                             ctocttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttcgcatag
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae
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Pred. No. 2e-105;
0; Mismatches 86;
                                                                                                                                                                                                                                                                                                                                                                                                                          1 (Pases 1 to 1173)
Du,M. and Ha,S.B.
Direct Submission submitted (22-APR-1997) Plant Biology,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Poa pratensis"
/strain="Glade"
/db_xref="taxon:4545"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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/codon_start=1
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Poa pratensis chitinase
AF000965
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/gene="Chi3"
194. .346
/gene="Chi3"
                                                                                                                                                                                                                                                                                                                   AF000965.1 GI:6164586
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Best Local Similarity 90.7%;
Matches 865; Conservative
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SOURCE
ORGANISM
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VERSION
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AUTHORS
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FYRYGAFIDAANSFGAFATTGGTDYRKREVAAFLAOUSHETTGGWPTAPDGPYSWGYC
FNQERGAPSDYCSPSSQWPCAPGKKYFGRGPIQISYNYNYGPAGRAIGTDLLNNPDLV
ATDATVSFKTALMFWATPQSPKPSSHDVITGRWSPSGADQAAGRYPGTGYJTNIINGG
LECGRGQDARVADRIGFYKRYCDLLGVSYGHNLDCYNQRPFA"
                                                                                                          /protein_id="AAG53609.1"
/db_xref="G1:12407647"
/translation="MRGVVVVAMLAAAFAVSAHAEQCGSQAGGATCPNCLCCSKFGFC
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   'chromosome="1"
                                              /note="cht9"
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Best Local Similarity 93.8
Matches 900; Conservative
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bukaryota, Viridiplantae, Streptophyta, Embryophyta, Trach
Spermatophyta, Magnoliophyta; Liliopsida, Poales; Poaceae,
Pooideae, Poeae, Poa.
To (Dases I to 1080)
Du.M. and Ha.A.
Direct Submission
                                                          GGGACCACGGGCGCCACCGACGTCAGGAAGCGCGAGGTGGCCGCCTTCCTCGCTCAGACC
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Poa pratensis chitinase (Chi2) gene,
AF000966
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28. .990
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YATDPTVSFKTALMFWAAGSPRPSSHAVITGGWSPSSAAQAAGTVPGTGTTINING
GLECGKGQDNRVADRIGFYKRYCDLLGVSYGNNLDCYSQRPFGS"
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                                                                                                                                                                                                           Length 1080;
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                                                                                                                                                                                                       Score 796.6; DB 8;
Pred. No. 7.2e-105;
0; Mismatches 99;
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89.6%;
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae, Oryza.

1 (bases 1 to 2808)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chitinase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (11-MAY-1993) to the DDBJ/EMBL/GenBank databases. Yoko Nishizawa, National Institute of Agrobiological Resources, Rice Genome Research Program: 2-1-2 Rannondai, Tsukuba, Ibaraki 305, Japan (E-mail:CS.SUZUKI/NFRI, Tel:0298-38-7451, Fax:0298-38-7408)
                                                                                                                                                                                                                                                                                                                                                                                                              841 gggcgcggcaggacggccg-----tgtcgccgaccggatcgggttctacaagcgctac 894
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721 aagcettegagecaegaegtgateaegggeeggtggageecetegggegeegaeeaggeg
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                                                                                                                                                 Oryza sativa (strain Nipponbare) DNA, clone RCG3.
Oryza sativa
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Rice Cht-3 gene for endochitinase,
D16223
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Nishizawa,Y.
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VASNATVSFRTALWFWMTAQSPKPSSHAVITGQWSPSSADQAAGRVPGYGVITNIING
GLECGKGQDNRVAVADRIGFYKRYCDLLGVSYGDNLDCYNESPFGSSAKRNIKRNIYY
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GNTSDYCGTGCQSQCNGCSGPTPVTPTPSGGGGVSSLVSQSLFEQMLLHRNDPSCQAN
GFYTYKAFIAAANSFAGFGTTGSTDVRKREVAAFLAQTSHETTGGWPTAPDGPYSWGY
                                                                                                                                                                                                                                                             Poa pratensis
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta, Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                                                             Pooldeae; Poeae; Poa.
1 (bases 1 to 1252)
Du,M. and Ha,S.B.
Direct Submission
Submitted (22-APR-1997) Plant Biology, U.C. Berkeley, Berkeley,
94706, USA
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     GGCAAAGGGCAGGACAACCGCGTCGCAGACCGGATCGGGGTTCTACAAGCGCTACTGCGAC
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                                     901 ctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttcg
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Pred. No. 3.7e-102;
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(Chil) gene,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Poa pratensis'/strain="Glade"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="chitinase"
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28. .1050
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AF000964
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28. .1050
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88.9%;
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/db_xref="G1:500617"
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REBNGNAAPTYCEPRFEWPCAGKFKYYFGRPPIGTTYNYGPAGQAIGSDLINNPDLV
ASDATYSFKTRAFWFWWTPQSFRPSCHAVITGGWTFSADDQAAGRYCF
RESNGNAAPTGGSFRPSCHAVITGGWTFSADDQAAGRYCF
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/evidence=experimental
1833 . 2795
/gene="cht-3"
                         National Institute of Agrobiological Resources
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Pred. No. 7.2e-82;
0; Mismatches 165;
Submitted (11-MAY-1993) to DDBJ by:
                                                                                                                                                                                                                                                                               /product="endochitinase"
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737 c 708 g 66
                                                                                                                              /organism="Oryza sativa"
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                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         /gene="Cht-3"
1833. "777-"
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/gene="Cht-3"
1887. .2792
/gene="Cht-3"
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ilarity 81.6%;
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Tsukuba, Ibaraki 305
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            Yoko Nishizawa
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Jurect Submission

Submitted (23-MAY-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail:tsasakieabr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7444, Fax:81-298-38-7468)

Tel:81-298-38-7444, Fax:81-299-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a "working draft' sequence."

* This sequence will be replaced
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Oryza sativa nipponbare (GA3) genomic DNA, chromosome 6, PAC
clone: P0548E04
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tactcctgggggctactgcttcaaccaggag---cgcggcgccacctccgactactgcacg
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Ehrhartoideae; Oryzeae; Oryza.
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* the accession number will be preserved.
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Oryza sativa
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Sasaki, T., Matsumoto, T. and Yamamoto, K. Direct Submission
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PROGRESS ***, in ordered pieces.
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AP003685.1 GI:14192855
HTG; HTGS_PHASE2.
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Pred. No. 1e-82;
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                                                                                    /clone="P0548E04"
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/organism="Oryza sativa"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
Location/Qualifiers
                                                                      /chromosome="6"
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TYTDAFVBAASAFRGFGTTGGTDTRREVBARLADQTSHETTGGWATAPDGAPAWGYC
FKQERGATSNYCTPSAQWPCAPGKSYTGRGPTQLSHNYNGPAGRAIGVDLLRNPDLV
AIDPFVSFKTAAWFWATAQAEKPSSHAVITGGWSPSGTDRAAGRYPGFGVIINIVNGG
IECGHGQDSRVADRIGFYKRYCDILGVGYGNNLDCYSQRPFA"
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Hordeum vulgare

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticeae; Hordeum.

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I (bases I to 1684)

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I solatius, S.M.J., Huang, J. and Muthukrishnan, S.
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66560, USA
19174 TACAAGCGCTACTGCGACATGCTGGGCGTCAGCTATGGCGATAACCTGGATTGCTACAAC 19115
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Direct Submission
Submitted (29-SEP-1993) Muthukrishnan S.,
Biochemistry, Willard Hall, Manhattan, KS
Location/Qualifiers
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Pred. No. 2.6e-81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /EC_number="3.2.1.14"
/function="hydrolyzes chitin"
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/product="chitinase"
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/organism="Hordeum vulgare"
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/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAA18586.1"
/db_xref="G1:495305"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="leaf"
/clone_lib="lambda GT11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /EC_number="3.2.1.14"
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503. .509
600. .1556
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/product="chitinase"
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/organism="Secale cereale"
/db_xref="taxon:4550"
                                                                                                                                                                                                                                                                                                                        /protein_id="BAB18519.1"
                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:11344587"
                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                         /product="seed
                                                                                                                                                                                                                                                                                           /codon_start=1
Ohnuma,T., Yamagami,T.
Cloning and Sequencing
Unpublished
                                                                                                                                                                                                                                    /gene="rsca"
58. 1003
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Spermatophyta; Magnoliophyta, Liliopsida; Poales, Poaceae,
Pooideae, Triticeae, Secale.
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                                                                                                          tecattatetegeagtegetettegaeeagatgetgetgetgeaeegaaegaegeggegtge
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                                                                                         the DDBJ/EMBL/GenBank databases. Takeshi
                                                                                                         Yamagami, Kyushu University, Protein Chemistry and Engineering, Froutly of Agriculture; Hakozaki, 6-10-1, Fukuoka, Higashi-Ku, Fukuoka 812-8581, Japan (E-mail:yamagami@uclink.berkeley.edu, rel:81-92-642-4218, Fax:81-92-642-3051)
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Chitinase
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of the Rye Seed
                                   2 (bases 1 to 1191)
Ohnuma.T., Yamagami,T. and Ishiguro,M.
Direct Submission
Submitted (22-NOV-2000) to the DDBJ/EM
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GSTSAYGGSGCQGGGGGTPPPSGGGGSGYASICSCONTLINENDACPA
KNEYTYDAFVAAANAPPSFATTGDAATRKRUVAAFLAGTSGTTGGAATAPDGPYSWG
YCFKEDWROWGSDYGSGSGGGGGGTPPPSGGGGSGYASICSTTGGAATAPDGPYSWG
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1318 . 1289
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1318 . 2286
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687 c 665 g 67
                                                     /evidence=experimental
                                                                                                                                  /EC_number="3.2.1.14"
                            /note="transcription
                                                                                                                                                                 /codon_start=1
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1 (Dases I to 2739)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chitinase genes
MOL. Gen. Genet. 241 (1-2), 1-10 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (sub_species japonica, strain Nipponbare) DNA, clone
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Nishizawa,Y.
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1918 AACTACAACTACGGCCCGGCGGGGCCATCGGCTCCAACCTGCTGAGCAACCCGGAC
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                 175 CAGTICGGCTGGTGCGGCTCCACCTCCGACTACTGCGGCCCGGATGCCAGAGCCAGTGC
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                                                        caatcacccaagcettegagecaegaegtgateaeggggeeggtggageeeetegggeege
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Zhu,Q. and Lamb,C.J.
Plant defense genes and plant defen
Patent: US 5695939-A 2 09-DEC-1997;
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Pred. No. 6.5
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Sequence 2 from patent US 5695939.
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Direct Submission
Submitted (18-SEP-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBICLOGICAL RESOURCES, ISUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
305, JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
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COGGGCOAGCAACTTCTACAACCTACGACGCCTTCGTCGCCGCCGCCGCCGCCTTCCGGG
                                                                   cttogogacoacaggtagcacogacgtcaagaagcgcgaggtggccgcgttcctcgctca
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Nishizawa,Y. and Hibi,T.
Isolation and characterization of a cDNA for rice Plant Sci. 76, 211-218 (1991)
Nishizawa,Y.
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O.sativa mRNA for endochitinase.
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Oryza sativa
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GYGVIINIVNGGLECGHGPDDRVANRIGFYQRYCGAFGIGTGGNLDCYNQRPFNSGSS
VGLAEQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Enrhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 1186)
Nishizawa,Y., Kishimoto,N., Saito,A. and Hibi,T.
Sequence variation, differential expression and chromosomal location of rice chitinase genes
Mol. Gen. Genet. 241 (1-2), 1-10 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (13-NOV-1990) Y. Nishizawa, NATIONAL INSTITUTE OF
AGROBIOLOGICAL RESOURCES, TSUKUBA SCIENCE CITY, KANNONDAI, IBARAKI
                                                                                                                   781
                                                                                                                                                                                        841
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                                                 662 GGATGACGCCGCAGTCGCCCAAGCCGTCGTGCCACGCGGTGATGACAGGGCAGTGGACGC
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endochitinase.
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/organism="Oryza sativa"
/strain="japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
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10. .1032
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106. 228
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10. .105
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Nishizawa,Y.
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TTGDATRKREVAAFLAQTSHETTGGMATAPDGPYSGGYCEKEENNGNVGSDYCVQSS
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                                                                                                                                                                                          /translation="EQCGSQAGGALCPNCLCCSQYGWCGSTSAYCGSGCQSQCSGSCG
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81.0%; Pred. No. 1.5e-78;
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                                                                                                    /codon_start=1
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polyA_site
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XEENNGNAPTYCEPRPWAFCAARKYYGGFIGFIGWTSTADDQAGRYGGTGNIINGCVE
CGHGADDKVADRIGFYRRYCDMLGVSYGDNLDCYNQRPYPPS"
                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 1237)
                                                                                                                                                                                                                                                                                                                                                                   Huang J.K., Wen L., Swegle, M., Tran, H.C., Thin, T.H., Naylor, H.M., Muthukrishnan, S. and Reeck, G.R.
Nucleotide sequence of a rice genomic clone that encodes a class
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                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (25-AUG-1990) Wen L., Western Illinois University,
Department of Chemistry, Currens Hall, Macomb, IL 61455, USA
2 (bases 1 to 1237)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAGCCAGTGCTCCGGCGGCGGCGGCGCCCCGACCCCGCCCTCCAGCGGTGGCGGC
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TCGGCACCGGCGGCAACCTCGACTACAACCAGAGGCCGTTC 996
                                                                                      OSCHIT 1237 bp DNA PLN
Oryza sativa (rice) gene for endochitinase.
X54367
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Plant Mol. Biol. 16 (3), 479-480 (1991)
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146. .1102
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Oryza sativa
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 /note="cysteine-rich di
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1150. 1153
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77.9%;
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                                                                                          /dev_stage="seedlings"
                                                        /db xref="taxon:4530"
Location/Qualifiers
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390. .893
368. .974
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TATA_signal
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1 (bases 1 to 2048)

Xu,Y., Zhu,Q., Panbangred,W., Shirasu,K. and Lamb,C.

Regulation, expression and function of a new basic chitinase gene in rice (Oryza sativa L.)

Plant Mol. Biol. 30 (3), 387-401 (1996)
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Institute, 10010 N. Torrey Pines Rd., Lo Jolla, CA 92037, USA
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                                                                                          485 GCCTACCGGGCTTCGCCACGCGCGACGCCGACGCCGACGCTGCAAGCGCGAGGTCGCCGCC
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1057. .1116
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1057. .2025
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/EC_number="3.2.1.14"
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1476 GACGTCGCACGAGACCATGGGCGGGGGGGCGCGCCCCGATGGCCCCTACTCGTGGGG 1535
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30	595
477 ctactgetteaaceaggagegegegecaceteegaetaetgeaegeegagete 530	1536 CTACTGCTTCAAGGAGGAGAACAACGCCAACGTTGGGTCCGACTACTGTGTCCAGAGCTC 1595
aaccaggagcgcggccacc	 AAGGAGGAGAACAACGGCAACGTTG
7 ctactgcttca	6 CTACIGCTIC
Oy 47	Db 153

QQ

Qy Db

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⁷¹¹ gcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccttcgggcgc 770

QQ QΥ

 $Q\underline{\mathbf{y}}$ qq

⁹⁵¹ gttc 954 $Q_{\overline{\Lambda}}$

²⁰¹³ TITC 2016

Search completed: May 3, 2002, 15:39:33 Job time: 4662 sec

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3, 2002, 16:32:50 ; Search time 309.71 Seconds (without alignments) 2657.429 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	Description	Rye chitina	RCH10 chiti	Rice chitinase RCH	Nucleotide	cDNA encodi	Sequence en	Floral orga	Banana ripening fr	Sequence en	Chitinase coding's	Full length chitin
		4889	1408	1346	4983	6224	2518	9982	5613	5264	AAT79940	9941
	ΩÏ		3 AAQ3	5 AAQB	2 AAF5	1 AAA9				1 AAQ0		
	DB	20	H	H	7	2	15	19	20	H	18	
	Query Match Length DB	954	1151	1151	3035	1163	1002	1318	7397	4704	879	998
æ	Query	0.68	64.0	64.0	63.7	62.5	53.5	46.0	39.5	39.0	38.5	10 00 10
	Score	854.6	614.6	614.6	611.4	600.2	513.6	441.4	379.2	374.4	369.2	369.2
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American elm chiti	Nicotiana sp. intr	edneuce	Banana fruit ripen	fruit	cDNA encoding a ma	Banana fruit ripen	cDNA encoding a ma	Rye chitinase-like	encodin	Banana fruit ripen	Banana fruit ripen	c	dopsis t	Floral organ-speci	a fruit	lectin	Urtica dioica aggl	PR-Q cDNA cloned i	Tobacco PR-Q gene.	CO PR-Q	PR-Q protein encod	PR-P cDNA cloned i	CO PR-P	PR-P protein encod	\circ	Endochitinase prec		Sequence of chimer	-tobacco e		Petunia hybrida ex	cDNA sequence enco
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17	18	21	20	20	21	20	21	20	21	20	20	21	21	19	20	21	22	11	10	20	20	11	20	20	13	15	13	13	15	12	18	21
1225	1152	1152	721	755	1118	802	1013	756	583	768	769	1077	991	2636	730	1317	1317	1010	1020	1020	1020	896	968	968	1153	1153	1160	1863	1863	965	996	996
37.3	36.2	36.2	33,6	33,4	32.1	32.0	31.9	31.4	28.6	27.1	27.0	25.6	23.1	21.2	20.2	19.4	19.4	18.5	18.5	18.5	18.5	18.5	18.5	18.5	18.1	18.1	18.1	18.1	18.1	17.6	17.6	17.6
358	347.6	47	323	320.8	90	307	306	301.4	74	260	259.2	246				186.6		178	178	178	178	77	7	77	73	73	73	7	7.3	59	169.2	59
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ALIGNMENTS

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The present sequence encodes winter rye (Secale cereale L. cv. Mustater) CHF9 preprotein (see AMW98079). Mature CHF9 (see AAW98080) is a chitinase-like protein that has chitinase (antifugal) and antificeaze activities. CHF9 DNA (ch-9) was obtained by isolating preprotein that has chitinase (antifugal) and strong many plants grown at low temperatures in the absence of pathogens or other stresses, i.e. under conditions when only chitinases with antifreeze activity would be expressed, and then sorting the cold-induced chitinase CDNAs to determine which encoded proteins with ice-binding ability. CHF9 and CHF46 (see AAW98081-82) have been cloned and expressed in bacterial and yeast (Pichia) systems and in Arabidopsis thaliana. The chitinase-like antifreeze microorganisms exposed to increase freezing tolerance of plants and microorganisms stooped to sub-zero temperatures; to inhibit ice recrystallisation in biological materials or foods; for metroorganisms exposed to sub-zero temperature of cells, embryos, tissues etc. (particularly human platelets); and to kill tumour cells. They are also used to inhibit initiation and progression of diseases or spoilage cused by low temperature pathogens

(particularly fund) in plants, frozen foods and any cryopreserved
                                                                                                                                                                  New nucleic acid encoding antifreeze polypeptides from plants -
particularly with chitinase activity, used to impart frost, and
pathogen, resistant to plants, for preservation of foods, cells etc.
and for treating tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 954 BP; 162 A; 335 C; 306 G; 151 T; 0 other;
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                                                             Xiong
                                                                                                                                                                                                                                                                              2; Fig 21a; 118pp; English.
                                                             щ
                                                             Moffatt
                                                                                                                           P-PSDB; AAW98079, AAW98080
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                  (ICEB-) ICE BIOTECH INC
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Matches 900; Conserv
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                                                           Griffith M,
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ä 240 360 tteggtttetgeggeaceaecteegaetaetgeggeaeeggetgeeagageeagtgeaat 180 361 gegaceacaggtageacegaegteaagaagegegaggtggeegegtteetegeteagaet 420 gagcaatgeggetegeaggeeggegggggegaegtgeeceaactgeetetgetgeageaag 120 Gaps 1 atgagagagttgtggtggtggtggccatgctggccgcggccttcgccgtgtctgcgcacgcc 60 1 atgagaggagttgtggtggtggccatgctggccgcggccttcgccgtgtctgcacacgcc 60 99ctgcagcggcggcaccccggtaccggtaccgacccctccggcggcggcgtctcctcc gccaaggggttctacaactacggcgccttcgtcgccgccgccactcgttctcgggcttc 180 --ccgctgcggcggcacaccagtaccggtaccgaccccaccggcggcggcgtgtcctcc .; m 89.0%; Score 854.6; DB 20; Length 954; 94.0%; Pred. No. 1.1e-143; 54; Indels 121 181 61 301 QQ g g g qq QYq Q ă Ω Y ă

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                                                                                                                                 657
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                                                                                                                                                                                                                                                     "Region conserved between class I and class II chitinases"
                                                                                                                      toggacgcgaccgtgtcgtttaagacggcgttgtggttctggatgacgccaatcaccc
                                                                                                                                                                                                                       aaaccttcgagccacgacgtgatcacgggccggtggagcccctcgggcgccgaccaggca
                                            tgetteaaceaggagegegegeeceeteegaetaetgetegeegagetegeagtggeeg
                                                                  tgtgcgccgggcaagaagtacttcgggcgcggggcccatccagatotcacacacaactacaac
                                                                                                             tacgggccggcgggggggggccatcggcaccgacctgctcaacaacccggaccttgtgggcg
                                                                                                                                                                            acggacgccaccgtgtcatttaagacggcactgtggttctggatgacgccgcagtcacca
                                                                                                                                                                                                  aagoottogagocacgacgtgatcacgggccggtggagccctcgggcgccgaccaggcg
                                                                                                                                                                                                                                                                                                            838 gggcgcgggcaggatgctcgtgtcgccgaccgaatcgggttctacaaagcgctactgtgac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; region; rice; chitinase; physical; biological; stress; leaves; stems; roots; male; female; reporter; monocotyledon; dicotyledon; development; plant; defence; selectable; genes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= c
/note=__Putative polyadenylation signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polyadenylation signal"
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55..1065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/note= "Putative
                                                                                                                                                                                                                                                                                                                                                                                                              AAQ31408 standard; DNA; 1151 BP
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1053..1058
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCH10 chitinase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-1992;
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AAQ31408
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The sequence given represents the rice chitinase gene. The promoter region of this gene (see AAQ31407) is responsive to physical and/or biological stress. The pattern of expression of this gene in mature plants is characteristic. There is a low level of expression in leaves, a moderate level in plant stems and the highest level in roots and the male and female parts of the plant. The chitinase promoter sequence may be linked to a reporter gene for expression in mono- or dicotyladon plants. Expression of this reporter gene may be used to study patterns of development and controlled expression of plant defence genes and selectable genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -aatggetgeageggeggeaceeeggtaeeggtaeegaeeeeeteeggeggeggegtete 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcgttcctcgctca
                                                                                                                                           DNA fragment contg. chitinase gene and its regulatory region responsive to mature plant stress and has low level expression leaves, moderate level expression in stem and high level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP; 197 A; 409 C; 353 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 614.6; DB 13;
Pred. No. 4.6e-101;
0; Mismatches 179;
                                                                                                                                                                                                                                       Disclosure; Page 33-34; 45pp; English
               BIOLOGICAL STUDIES
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ilarity 80.3%;
Conservative
                                                                                       WPI; 1992-415785/50
                                                                                                                                                                                                  expression in roots
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                 SALK INST
                                                                                                        P-PSDB; AAR29019
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Best Local S
Matches 773
                                                  Lamb CJ,
               (SALK)
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The SphI fragment of rice chitinase RCH10 gene (given in AAQ81346) and an alfalfa beta-1,3-glucanase coding sequence (AAQ81347) were
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                                                                                                                                                                                                                     ggagtgcggccatggcgaggacgatcgcatcgccgaccggatcggcttctacaagcgcta 950
                                                                                                                                                                                                                                             ctgcgacctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgtt 953
594 ctacaactacgggccggcgggggggggcatcggcaccgacctgctcaacaacccggacct
                     651 cttcaactacgggccggggggggggggcatggcgccgacctgctcggcgacccggacct
                                              tgtggcgtcggacgcgtgtcgtttaagacggcgttgtggttctggatgacgccgca
                                                                                                atcacccaagccttcgagccacgacgtgatcacgggccggtggagcccttcgggcgccga
                                                                                                                       771 gregeecaageegtegtgeaaegeggtegeeaeeggeeagtggaegeetteegeegaega
                                                                                                                                              cgagtgcggggcggggacggccgtgtcgccgaccggatcgggttctacaagcgcta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chitinase; RCH10 gene; transgenic plant; disease resistance; crop improvement; tobacco; Nicotiana tabacum; plant defense; fungus pathogen; Cercospora nicotinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transgenic plants contg. several plant defence associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 31-32; 45pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STUDIES
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/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                   BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rice chitinase RCH10 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thanatephorus cucumeris;
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P-PSDB; AAR67969.
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                                                                                                                                                                                                               cagttcggctggtgcggctccacctccgactactgcggcgccggatgccagagccagtgc
transgenic tobacco, nicotinae and
                                                                   Length 1151;
                                                                                        11;
                                                                                        Indels
                                       BP; 197 A; 409 C; 353 G; 192 T; 0 other;
                                                                   DB 16;
                                                                              .6e-101;
es 179;
 into vectors for co-expression in improved resistance to Gercospora
                                                                  Score 614.6; D
Pred. No. 4.6e-
O; Mismatches
                    Thanatephorus cucumeris fungal infection.
                                                                   64.0%;
ilarity 80.3%;
Conservative
                                                                               Similarity
                                       Sequence 1151
 incorporated resulting in
                                                                    Query Match
Best Local Simil
Matches 773; (
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The present sequence encodes a chitinase designated RCH10. The specification describes chimeric receptors which are used for modulating plant responses to pathogens. The receptors computise a heterologous extracellular domain (e.g. from a Bril protein or RCH10 protein) and a kinase domain (e.g. from disease resistance protein Xa21). The Xa21 gene is a member of disease resistance genes referred to as RKK genes. When Xa21 is present in a transgenic plant, it confers resistance to Xanthomonas spp. The plant receptors containing heterologous domains are useful for modulating plant responses to pathogens including viruses, bacteria, nematodes, fungi or insects. The nucleic acids can be used to
                                                                                                                                                                                                                                                                                                                                                                                                              chitinase;
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Pred. No. 1.7e-100;
0; Mismatches 181; Indels 11;
                                                                                                                                                                                                                                                                                                                                                                                                           RKK gene; transgenic plant; protein; RCH10 protein; ss.
                                                                                                                                                                                                                                                                                                                                                              Nucleotide sequence of a rice chitinase designated RCH10.
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CDNA; 1163

standard;

AAA96224

(first entry)

08-FEB-2001

AAA96224 AAA96224;

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The present sequence encodes a chitinase polypeptide. The specification describes glucosyl hydrolase family 19 chitinases (AAB18894, AAB18896, AAB18899, and ABB1890-015), and glucosyl hydrolase family 18 chitinases (AAB18895, AAB18957-98 and AAB18950-01). The level of chitinase in plants can be modulated to enhance disease resistance in crop plants and for control of pathogens. The chitinase polynucleotides are also useful as molecular markers for genotype in a plant, and for sequence
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                         Chitinase; glucosyl hydrolase family 19; glucosyl hydrolase famiy pathogen control; disease resistance; molecular marker; ss.
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cDNA encoding a maize chitinase polypeptide designated ZmCh7
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                                                                                                          Location/Qualifiers 32..817
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                                                                                Chet I, Mundy J,
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                                                                                                                                                                                                                                                                       caacggtgggctcgagtgcggggcgggcaggacggccgtgtcgccgaccggatcgggtt 881
                                          ctectgggggetaetgetteaaceaggagegegegeeect----eegaetaetgeae
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                                  cetegeteagaetteecaecgaegaegaeggegggtggeegaeggeeeegaeggeeeeta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antifungal; pathogen; resistance; transgenic organism; synergy; crop protection; transgenic plant; chitinase; glucanase; protein synthesis inhibitor; disease; ss.
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/note= "Putative polyadenylation signal."
  ggettegegaceacaggtageacegacgteaagaagegegag-
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This sequence encodes Chitinase G. Chitinase is an enzyme which breaks down chitin, the major protein in insect exoskeletons. The coding sequence may be used in the construction of transgenic organisms, especially plants, to produce pathogen resistant organisms. The genome of such transgenic organisms preferably contains more than one gene with pathogen inhibiting activity, each gene under the control of active promoters. The two gene products then show a synergistic increase in pathogen induced activity so that the transgenic organisms have a greater degree of resistance or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 53.5%; Score 513.6; DB 15; Length 1002; Best Local Similarity 81.1%; Pred. No. 4e-83; Matches 597; Conservative 0; Mismatches 139; Indels 0;
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                                                                                                                                                                                                 Logemann
                                                                                                                               (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resistance against a wider spectrum of diseases.
                                                                                                                                                                                             Jach G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 13-14; 19pp; German
                                                                                                                                                                                          Sornhardt B, Goernhardt B;
                                                                                                                                                                                                 Gornhardt
92DE-4234131
                                                              92DE-4234131
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P-PSDB; AAR52577.
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Schellj,
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46.08;
                            Best Local Similarity 70.6 Matches 684; Conservative
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               Query Match
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                                                                                                                                                                                 943
763
                              667
                                                                                                                                                                                                               847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floral-organ specific gene; chitinase; promoter; Oryza sativa; rice; flower part; monocotyledonous plant; bacterial resistance; ds.
                                                                                                                                                                                                  tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccct
                            tgacggcgcagccgagccatcgagccatgctgtgatcgccggccagtggagcccgt
                                                                                                                        acggtgggctcgagtgcgggggggggggggggggcgtgtcgccggaccggatcgggttct
                                                                                                                                                   acggcgggatcgagtcacgggcaggacagccgcgtcgccgatcgaatcgggtttt
                                                                                                                                                                                   acaagcgctactgcgacctccttggcgtcagctacggtgacaacctggactgctacaacc
                                                          /product= "floral-organ specific chitinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Promoter sequence associated with chitinase, specific to organs - allows expression of genes in the flower parts o
                                                                                                                                                                                                                                                                                                                                                                                                                                        organ-specific chitinase encoding cDNA
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                                                                                                                                                                                                                                                                          agagaccettegeeta 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monocotyledonous plants
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P-PSDB; AAW64776.
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AAV49982

Sequence 1318 BP; 231 A; 442 C; 440 G; 205 T; 0 other;

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Length 1318;
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Pred. No. 2.6e
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                                                                                                                                       Banana; fruit ripening; differential expression; fruit development;
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Pred. No. 2.8e-59;
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                                                                                                                                                                                                                                                                                                                          (BOYC-) BOYCE THOMPSON INST PLANT RES.
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                          AAX25613 standard; DNA; 7397 BP.
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63.9%;
                                                                                                            Banana ripening fruit Endo.
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                                  cgetettegaccagatgetgetgeaccgeaacgacgeggegtgeetggecaaggggttet
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Sequence 879 BP; 216 A; 221 C; 242 G; 200 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                 Length 4704;
                                                                                                                                                                                      Recombinant DNA contg. high level promoter and plant chitinase gene - for transforming plants to over:express chitinase, imparting resistance to phytopathogenic fungi.
                                                                                                                                                                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                             or dicotyledons to show increased resistance to fungal attack. A high level promoter is used from CMV 35s or 19s complement, NOS or OGS promoters of Agrobacterium opine synthetase gene, the RUBISCO small unit or the chlorophyl A/B binding protein.
                                                                                                                                                                                                                                                                   Sequence encoding chitinase may be used to transform mono-
                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 281; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Score 374.4; DB 11;
Pred. No. 2e-58;
                                                                                                 (DUPO ) DU PONT DE NEMOURS CO
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Similarity 65.6%;
                                                                        88US-0285252
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                                                                                                                                                   WPI; 1990-224529/29
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This sequence represents the coding sequence for the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fungi. Plants have this enzyme to protect themselves from pathogenic fungi. Thus this enzyme can be used to prevent plants from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease
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                                                                                               (NIHA ) JAPAN ENERGY CORP.
(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER.
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(first entry)

Location/Qualifiers 1..879 /*tag= a

chitinase

/*tag= a /product=

95JP-0347367 95JP-0347367

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Chitinase; pumpkin; enzyme; decompose; plant cell membrane; peptidase; fungal cell membrane; pathogenic fungus; disease resistance; chitin; ss.
                                                                                                                                                                                                                                                                                                                                                   Chitinase derived from pumpkin - used to protect plants against
                                                                                                                                                                                                                                                                          (NIHA ) JAPAN ENERGY CORP.
(SEKI-) ZH SEKIYU SANGYO KASSEIKA CENTER
                       Full length chitinase coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                      Claim 3; Page 4-5; 36pp; Japanese.
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                       Length 879;
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                       DB 18;
                      Score 369.2; DB 18;
Pred. No. 1.8e-57;
0; Mismatches 293;
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nilarity 65.2%;
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This sequence represents the coding sequence for the pumpkin chitinase. Chitinase is an enzyme decomposing chitin (not present in plant cell membranes) found in the cell membranes of fund. Plants have this enzyme to protect themselves from pathogenic fungi. Thus this enzyme can be used to prevent plants from being infected with pathogenic fungi, and the chitinase gene can be introduced into plants to improve their resistance to diseases caused by fungi. As the amino acid sequence of the chitinase does not have any region to be cleaved by ubiquitous peptidases in cells, the chitinase produced by genetic recombination technology works for various host cells and serves for plant immunity to confer disease
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Pred. No. 1.8e-57;
); Mismatches 293; 3
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ilarity 65.2%;
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                                                                                                                                                                                 aagcettegageeacgaegtgateacgggeeggtggageeetegggegeegeegaeeaggeg 780
                                                                                                                                                            tacgggccggcgggcaggccatcggcaccgacctgctcaaccaggaccttgtgggcg
                                                                                                                                   523 tacgggccagcgggtagggcgctaaatttgaatttgctgaacaaccctgatttggtagcc
                                                                                                                                                                                          geggggagggtgeetgggtaegggtgtgateaecaacateateaaeggtgggetegagtge
                                                      tgetteaaceaggagegegeeaceteegaetaetgeaegeegagetegeagtggeea
                                                                                      teccaegagaegaeeggggtggeegaeggeeeegaeggeeeetaeteetgggggetae
                                      346 teteatgaaaceaetggagggtgggetaeggeaeeggatggeeeatatgegtggggatat
                                                                      tgcttcataagggag---agaaaccaagacgtatattgctcacctaaccagcaatggccg
                                                                                                                                                                                                                                                                                      ctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttc 954
                                                                                                                                                                                                                                                                                                                                                                                                Clone pHS2; chitinase; american elm; fungus; Ophiostoma ulmi; dutch elm disease; E. coli; chitinase-like protein; fungal infection; ss.
                                                                                                                                                                                                                                                                                                                                                                                 American elm chitinase-like protein coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chitinase-like protein
                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
88..150
                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                   AAT33325 standard; DNA; 1225
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1153..1158
/*tag= e
1168..1177
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/product= (
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151..1038
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88..1041
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                                                                                                                                                                                                                                                                                                                                                                                                                                American elm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       sig_peptide
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This sequence represents the CDNA clone pHS2, which encodes a protein having chitinase-activity derived from american elm. This protein inhibits the fungus Ophiostoma ulmi, the causative agent of dutch elm disease. The clone pHS2 may be used to transform E. coli cells for the recombinant production of the chitinase-like protein. The protein may be used in a composition to inhibit fungal infection of elm trees.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 ttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcgttcctcgctcag 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           actteceatgaaactacaggtgggtgggcaagtgcaccegaeggtecatactettgggga 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tactgcttcaaccaggagcgcggcgccacctccgactgcacgccgagctcgcagtgg 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccatgtgcgccgggcaagaagtacttcggggcgcgggcccatccagatctcacacaactac 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          googagcaatgoggotogcaggccggcgggggggggcgacgtgccccaactgcctctgctgcagc 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gcagagcaatgtggaagccaagctgggggtgcagtgtgtcccgttggggctctgctgcagc 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aagtteggtttetgeggeaceaecteegaetaetgeggeaeeggetgeeagageeagtge 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggcggcagcggtagcgat-----gacattggc 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 tecattatetegeagtegetettegaecagatgetgetgeacegeaaegaegegegtge 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  295 ggtctcatatcaagctccgcctttaatgacatgcttaagcatcgtaacgacggtggttgt 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aactacgggccggcgggcaggccatcggcaccgacctgctcaacaacccggaccttgtg 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33;
                                                                                                                                                                                                                                                                                                                Isolated chitinase gene derived from an American elm - used to obtain prods. for inhibiting fungal infection of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1225 BP; 322 A; 277 C; 313 G; 313 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 358; DB 17;
Pred. No. 1.7e-55;
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 1; 12pp; English.
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64.0%;
                                                94US-0286020
                                                                                            94US-0286020
                                                                                                                                          (UNMS ) UNIV MICHIGAN STATE
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Matches 575; Conservative
                                                                                                                                                                                          Sticklen MB;
                                                                                                                                                                                                                                         WPI; 1996-353879/35
                                                                                                                                                                                                                                                                       P-PSDB; AAW00186
                                                04-AUG-1994;
                                                                                              04-AUG-1994;
23-JUL-1996
                                                                                                                                                                                             Hajela RK,
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Best Local S
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0 other;

315 T;

C; 283 G;

281 A; 273

Sequence 1152 BP;

SS

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tgcgggcgcgggcaggacgtgtcgccgaccggatcgggttctacaagcgctactgc 897
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                                                                                                                                                                                                                                                                                                                                                                                                                    gacctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttcg 955
                                                                                              geggegggagggtgcctgggtacggtgtgatcaccaacatcatcaacggtgggctcgag
                                                                                                                                                                                                                                                        835 teggecegacegagttgegggetaeggegtgateaceaacattateaaeggtgggatagaa
gogteggaegegaeegtgtegtttaagaeggegttgtggttetggatgaegeegeaatea
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JF;
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/product= intracellular_chitinase
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Woloshuk
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10..984
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, Vloemans AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 1152
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RIJKSUNIV TE LEIDEN.
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P-PSDB; AAR13275.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ12898 standard;
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Sela-Buurlage MB,
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                                                                                                                                                                                                                                                                                                                        642 caatectgatttagtggccacagatecagtaatetcattcaagtcagetetetggttttg
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                                                                                       cetetgetgeageaagtteggtttetgeggeaceaceteegactaetgeggeacegge--
                                                                                                                                                       tigecagagecagtgecetggtggtccca------caccaccgg
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                     24;
  Length 1152;
  12;
 ; DB 1.
                       0; Mismatches
Score 347.6;
Pred. No. 1.2
tch 36.2%; al Similarity 63.2%; 580; Conservative
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  Query Match
Best Local S
                       Matches
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RESULT

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                                                                                                                                                                      Intracellular chitinase, antifungal, transgenic plant; synergism; beta-1,3-glucanase gene; tobacco; ss.
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63.2%; Pred. No. 1.2e-53;
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                                                                                                                                                                                                                                                                                                                                                                                             /product= intracellular_chitinase
                                                                                                                                 Nicotiana sp. intracellular chitinase cDNA.
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                         BP
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                         CDNA; 1152
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New transgenic plants expressing chitinase and glucanase have improved resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
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                                                                                                                                                                                                                                            Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
oshuk CP, Bol JF, Linthorst HJM, Van Roekel JSC;
                                                                                                                                                                                                                                                                                                                                                                                                                              present sequence encodes an extracellular chitinase, The
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/product= "chitinase"
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P-PSDB; AAB07513.
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Search com Job time: 7. 401 461 -tgccagagccagtgcaatggctgcagcggcggcacccggtaccggtaccgacccctc cggcggcggcgtctcctccattatctcgcagtcgctcttcgaccagatgctgctgcaccg 222 tggtggggatctcggcagtatcatctcaagttccatgtttgatcagatgcttaagcatcg caacgataatgcatgccaaggaaagggattctacagttacaatgcctttatcaatgctgc 342 taggicititiceiggetitiggiaciagiggigataceacigeeegtaaaagagaaatege occetactectgggggtaetgetteaaceaggagegegegegeecteegaetaetgeae -----caccaccgg caacgacgcggcgtgcctggccaaggggttctacaactacggcgccttcgtcgccgc caactcgttctcgggcttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggtggc Score 347.6; DB 21; Length 1152; Pred. No. 1.2e-53; 183 ttgccagagccagtgccctggtggtccca-----36.2%; Best Local Similarity Query Match 282 342 402 402 282 163 222 462

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581 641 641 701 701 761 761 821 821 881 881 941 882 ttacaggaggtattgcagtattcttggtgttagtcctggtgacaatcttgattgcggaaa 941 462 tecatacgegtggggttactgetggettagagaaaaatgtageeceeggegaetaetgtae 522 geogagetegeagtggceatgtgegeegggeaagaagtaetteggggegegggeeeateea gateteacaacaactacaactacgggccggcggggggaggccatcggcaccgacctgctcaa caaccoggaccttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctg caatcotgatttagtggccacagatccagtaatctcattcaagtcagctctctggttttg ctcgggcgcccgaccaggcggcgggggggggggcctgggtacggtgtgtcaccaacatcat 762 atogicigetgaccgcgcagccaaicglictccciggaiiiggigicaicacgaacaicai caacggtgggctcgagtgcggggcgcgggcaggacggccgtgtcgccgaccggatcgggtt caatggtggcttggaatgtggtcgtggcactgactcaagggtccaggatcgcattgggtt 522 accaagtggtcagtggccttgtgctcctggtcggaaatatttcggacgaggccccatcca ctacaagcgctactgcgacctccttggcgtcagctacggtgacaacctggactgctacaa ccaaaggccgttcgcata 959 702 762 822 822 642 702 942 δy q δž d δy g ŏ q δ qq QΥ q QΣ $^{\circ}$

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to construct a transgenic plant in a novel method to produce plants resistant to fungal attack. Such transgenic plants expressing an intracellular plant chitinase gene and a plant beta-1,3-glucanase gene within its tissues are predicted to exhibit improved resistance to pathogenic fundi. Such genes should be operably linked to promoters and terminators and optionally a gene encoding a selectable or screenable trait. Plants that overexpress the chitinase and glucanase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cctotyctycaycaagttcgytttctycgycaccacctccyactactycgycaccggc-- 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This cDNA sequence encodes an intracellular chitinase which is used
                                                                                                                     antifungal; transgenic plant; synergism; tobacco; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 347.6; DB 18; Length 1152; Pred. No. 1.2e-53; 0; Mismatches 314; Indels 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĽS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sungus-resistant transgenic plants - containing genes intracellular chitinase and beta-1,3-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1152 BP; 281 A; 273 C; 283 G; 315 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linthorst HJM, Melchers
age MB, Van ROEKEL JSC;
                                                                                                                                                                                                                                                                                  /product= intracellular_chitinase
                                                                                           Nicotiana sp. intracellular chitinase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               exhibit a synergistic antīfungal effect.
                                                                                                                                                                                      Location/Qualifiers
10..984
/*tag= a
10..78
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Woloshuk CP;
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              CDNA; 1152
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                                                                   (first entry)
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Matches 580; Conservative
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RIJKSUNIV LEIDEN.
                                                                                                                     chitinase;
                                                                                                                                  beta-1,3-glucanase gene;
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P-PSDB; AAW31297.
            AAT89952 standard;
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                                                                                                                     Intracellular
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Meulenhoff
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QQ δ g 14

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The present sequence encodes an extracellular chitinase. The specification describes transgenic plants which express a chitinase gene and a glucanase gene. The expression of the chitinase and beta-1,3-glucanase genes produces an antifungal effect. The transgenic plants are useful for improving plant resistance to pathogenic fungir. The recombinant polynuclectides and the process are useful for producing fungal resistant plants.
                                                                                                                                                                                                                                                                                                                                            improved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                      New transgenic plants expressing chitinase and glucanase have improve resistance against pathogenic fungi, particularly against Alternaria alternata or Fusarium oxysporum f. sp. lycopersici
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                                                                                                                                                                                                                                                Melchers LS, Meulenhoff EJS, Sela-buurlage MB;
Oshuk CP, Bol JF, Linthorst HJM, Van Roekel JE
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/product= "chitinase"
10..78
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63.2%;
                                                                                                                                97US-0801563,
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91US-0647831.
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Matches 580; Conservative
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                                                                                                                                                                                                                                                                Vloemans AA,
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                           sig_peptide
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641 701 941 581 581 582 aatttcacaactacaactacggaccttgtggaagagccataggagtggactcctaaa 641 642 caatcctgatttagtggccacagatccagtaatctcattcaagtcagctctctggttttg 701 761 761 821 821 882 ttacaggaggtattgcagtattcttggtgttagtcctggtgacaatcttgattgcggaaa 941 tecatacgcgtggggttactgctggcttagagaacaatgtagccccggcgactactgtac 521 caacggtgggctcgagtgcggggcgcgggcaggacggccgtgtcgccgaccggatcgggtt 881 caatggtggcttggaatgtggtcgtggcactgactcaagggtccaggatcgcattgggtt 881 762 ctcgggcgccgaccaggcggcgggggggggtgcctgggtacggtgtgatcaccaacatcat atogrategetgacegegecaategtetecetggatttggtgtcateacagaacateat gatgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagccc gatgactcctcaatcaccaaaaaccttcttgccacgatgtcatcattggaagatggcaacc ctacaagcgctactgcgacctccttggcgtcagctacggtgacaacctggactgctacaa gccgagctcgcagtggccatgtgcgccgggcaagaagtacttcggggcgcgggcccatcca gateteacacacactacaactacgggecgggggggggggccateggcacegacetgeteaa caacccggaccttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctg ccaaaggccgttcgcata 959 522 702 822 642 702 762 822 942 942 qq g q g δy g δŽ δž δŽ δ δŽ g

Search completed: May 3, 2002, 16:33:40 Job time: 7054 sec

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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
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CITY: Los Angeles
STATE: California
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NAME/KEY: CDS
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1526.282 Million cell updates/sec
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Sequence 15, 2
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                                              May 3, 2002, 16:27:02; Search time 142.45 Seconds
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Copyright (c) 1993 - 2000 Compugen Ltd
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Listing first 45 summaries
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GENES AND PLANT DEFENSE REGULATORY
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ZIP: 90071-2921
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CCMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/704,288C
FILING DATE: 22-MAY-1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: RELEAT, Stephen E.
REGISTRATION NUMBER: 31,192
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Pred. No. 1.6e-112;
0; Mismatches 179;
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CORRESPONDENCE ADDRESS:
ADDRESSEB: PRETTY, SCHROEDER, BRUEGGEMANN &
STREET: 444 South Flower Street, Suite 2000
US-08-455-736-7
US-08-971-217-7
US-08-91-81-270-12
US-08-449-08-12
US-08-449-08-12
US-08-456-265A-12
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US-08-455-416-12
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REFERENCE/DOCKET NUMBER: P31 8899
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/07704288C
Patent No. 5399680
GENERAL INFORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: PLANT DEFENSE
TITLE OF INVENTION: ELEMENTS
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Sequence 1, Application US/08093372

RESULT 2 US-08-093-372-1

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                                                                                                                       PLANTS CONTAINING MULTIPLE
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                                                                                                                                                                                                    Clark
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Pred. No. 1.6e-112;
0; Mismatches 179;
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                                                                                                                                                                                                                                                                                                                                                                                                       #1
                                                                                                                                                                                                  E: Pretty, Schroeder, Brueggemann & 444 South Flower Street, Suite 2000
Patent No. 5530187
GENBRAL INFORMATION:
APPLICANT: Lamb, Christopher J.
APPLICANT: Lamb, Oun
APPLICANT: Maher, Eileen A.
APPLICANT: Maher, Eileen A.
TILLE OF INVENTION: TRANSGENIC PLANTS CONTAIN
TITLE OF INVENTION: DISEASE RESISTANCE GENES
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atgagagagttgtggtggtggccatgctggccgcggcct-
                                                                                                                                                                                                                                                                                                                                                                                                       Version
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/093,372
FILING DATE: 16-UUL-1953
CLASSIFTOATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9391
                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DGS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31,192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Relter, Stephen E.
REGIGTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 64.0%;
Best Local Similarity 80.3%;
Matches 773; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1151 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619-546-9392
                                                                                                                                                                                                                                                             STATE: CA
COUNTRY: U.S.A.
ZIP: 90071-2921
COMPUTER READABLE FORM:
                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                     STREET: 444 South
CITY: Los Angeles
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 614.6; DB 1;
Pred. No. 1.6e-112;
0; Mismatches 179;
                    07/704,288
                                                                                             REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 546-4737
TELEFAX: (619) 546-9392
                                                                                                                                                                                                                                                                                                                                        DNA (genomic)
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80.3%;
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LENGTH: 1151 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPDLOGY: unknown
MOLECULE TYPE: DNA (genomic
                APPLICATION NUMBER: US 0° FILING DATE: 22-MX-1991
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 80.3 ses 773; Conservative
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           ), NAME/KEY: CDS
; LOCATION: 55..1062
US-08-379-259-2
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Matches
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                                                     CTTCGCCGCCGCGGCGACGCCGACAACAAGCGCGAGGTCGCCGGGTTCCTTGCGCA
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                      cttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcggttcctcgctca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENES AND PLANT
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APPLICATION NUMBER: US/08/379,259
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFENSE REGULATORY ELEMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/08379259
Patent No. 5695939
GENERAL INPORMATION:
APPLICANT: LAMB, CHRISTOPHER J.
APPLICANT: ZHU, QUN
TITLE OF INVENTION: DEFENSE GE
TITLE OF INVENTION: DEFENSE REGULATO
TITLE OF INVENTION: ELEMENTS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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OTHER INFORMATION: sequence' FEATURE:
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81.1%;
                                                                                                                                     FEATURE:
NAME/KEY: polyA_signal
LOCATION: 905..910
OTHER INFORMATION: /note
OTHER INFORMATION: signa
                                                                                                                                                                                                                               NAME/KEY: sig_peptide
LOCATION: 64..294
CTER INFORMATION: Anota
OTHER INFORMATION: seque
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: Anota
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                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: sig_peptide
LOCATION: 349..378
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LOCATION: 466..588
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; LOCATION: 133..861
US-08-457-797A-9
   OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity
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                                                                                                        774 ccaggcggcgggggggggggcctgggtacggtgtgatcaccaacatcatcaacggtgggct
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                                                atcacccaagccttcgagccacgacgtgatcacgggccggtggagcccttcggggcgccga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transgenic pathogen-resistant organism 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Graves, Donohue and Raymond
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/function= "chitinase"
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FILING DATE: June 1, 1995
ATTONNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REGISTRATION NUMBER: 35,225
REPERBNCE/DOCKET NUMBER: A29542 FWC -
TELECHOUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A29542 FWC
                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/08457797A Patent No. 5689045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Brumbaugh, Graves
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (***.
TELEFAX: 188555
TELEX: 188555
INFORMATION FOR SEO ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
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LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
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TITLE OF INVENTION:
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LOCATION: 1..63
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/product- "26 kD preprotein of chitinase G (ChiG)" /hote- "antifungal activity, especially on Trichoderma reesil and Fusarium sporotrichoides as well as Rhizoctonia solani and Botrytis cinerea."
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signal"
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LOCATION: 607..86
CHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                         /note= "probable signal peptide sequence"
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OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
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                                                                                        FEATURE:
NAME/KEY: 3'UTR
LOCATION: 662..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3'
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Pred. No. 9.5e-93;
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NAME/KEY: sig_peptide
LOCATION: 298.312
OTHER INFORMATION: /not
OTHER INFORMATION: sequ
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Best Local Similarity 81.1<sup>1</sup>
Matches 597; Conservative
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LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: see
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; LOCATION: 133..861
US-08-812-025-9
                                                                                                          LOCATION: 64..861
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
5'UTR
1..63
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FEATURE:
                                                                                     NAME/KEY:
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                                                                                                                                                                                                                                    704 tgaegeegeaateaeceaageettegageeaegaegtgateaegggeeggtggageeet
      teteacacaactacaactacgggccgggggggggggcatcggcaccgacctgctcaaca
                                    TGACGGCGCAGCCGCCCAAGCCATGCCATGCTGTGATCGCCGGCCCGGTGGAGCCGT
                                                                                                                      acccggaccttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -37/31335
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5804184
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Transgenic pat
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A22
TELECOMMUNICATION INFORMATION:
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TELEFAX: (212) 765-2519
TELEX: 23855
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Hordeum vulgare STRAIN: L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: cDNA ORIGINAL SOURCE:
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FEATURE:
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US-08-812-025-9
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STATE:
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/codon_start= 64
/function= "chitinase"
/function= "achitinase"
/product= "26 KD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
/richoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                403
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LOCATION: 862..1002
OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
FEATURE:
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LOCATION: 905..310
OCCATION: 055..310
OTHER INFORMATION: /note= "potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: sig_peptide
LCGATION: 349..378
OTHER INFORMATION: Sequence"
OTHER INFORMATION: sequence"
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CCGATION: 466..58
OTHER INFORMATION: Note= "probable signal peptide
OTHER INFORMATION: sequence"
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LOCATION: 607..861
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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sequence"
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Pred. No. 9.5e-93;
0; Mismatches 139;
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                     668 CAGGGGCTGACCGGGCCGCAGCCGGGTGTGGTGTGTGATCACCCAACATCATCA 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     428 cgagogoacaarigeccergececceggaageceracracegeceggecaarccaec 487
                                                                                                                                                                                                                                                          704 tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagccct 763
                                                                                                                                          488 TCTCCCACAACTACAACTATGGACCTGCCGGGCCCATCGGGGTCGATCTGCTGGCCA
                                                                                                                                                                                                                                                                                    608 TGACGGCGCAGCCCAAGCCATCGAGCCATGCATGCTGTGATCGCCGGCCAGTGGAGCCGT
                                                     cgagetegeagtggeceatgtgegeeggggeaagaagtaetteggggegegggeeeateeaga
                                                                                                                                                                                         644 acccggaccttgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctgga
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                                                                                                                      584 tottoacaacaactacaggccggcggggggggggggcatcggcaccgacctgctcaaca
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A29542 FWC - 37/31335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/09/138,873A FILING DATE: AUGUST 24, 1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09138873A Patent No. 6271438 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Baker & Botts
STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Tenser, Arthur REGISTRATION NUMBER: 18,839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: A2
TELECOMMUNICATION INFORMATION:
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(212) 765-2519
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     944 aaaggccgttcgcata 959
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                848 AGAGACCTTCGCCTA 863
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NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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: New York
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Ne..
STATE: New YO'
COUNTRY: U.S
TTO: 10112
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US-09-138-873A-9
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/function= "chitinase"
/function= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
Trichoderma reesil and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 goggoggogtotoctoattatotogoagtogotottogacoagatgotgotgoacogoa 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 ACGACGCCTGCCAGGCCAAGGCTTCTACACCTACGACGCCTTCGTCGCCGCGCA 247
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OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
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Pred. No. 9.5e-93;
0; Mismatches 139; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "potential polyadenylation
signal"
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sequence"
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OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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sequence"
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sequence"
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sequence"
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81.1%;
                                                                           Hordeum vulgare
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LOCATION: 905..910
OTHER INFORMATION: /not
OTHER INFORMATION: sign
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LOCATION: 466..588
OTHER INFORMATION: /no
OTHER INFORMATION: seq
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Best Local Similarity 81.1
Matches 597; Conservative
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607..861
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LOCATION: 64..294
OTHER INFORMATION: /nc
OTHER INFORMATION: sec
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LOCATION: 298.312
OTHER INFORMATION: /nc
OTHER INFORMATION: Sec
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LOCATION: 349..378
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133..861
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
                                    CDNA
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OTHER INFORMATION:
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                    linear
                                                                                                                                    5'UTR
1..63
                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: 3'UTR
                                    MOLECULE TYPE: CORIGINAL SOURCE: ORGANISM: Hord
                                                                                                                                                                                           NAME/KEY: CDS
STRANDEDNESS:
TOPOLOGY: lin
                                                                                             STRAIN: L.
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NAME/KEY:
LOCATION:
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US-09-138-873A-9
                                                                                                                                    NAME/KEY:
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HAPLOTYPE:
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                                                                                                                  LENGTH:
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                       tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccct
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                                                                                                                              cgagetegeagtggeeatgtgegeegggeaagaagtaettegggeeggggeeeateeaga
                                                                                                                                                                                 teteacacaactacaactacgggccggcggggggggggcateggacctgeteaaca
                                                                                                                                                                                                accoggacettgtggcgtcggacgcgaccgtgtcgtttaagacggcgttgtggttctgga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Masomeh B. Sticklen and Ravindra K. Hajela
TITLE OF INVENTION: A Chitinase cDNA Clone From a
TITLE OF INVENTION: Disease Resistant American
TITLE OF INVENTION: Elm Tree
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/286,020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Acer
OPERATING SYSTEM: MS-DOS 5.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/08286020 Patent No. 5539095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Okemos
STATE: Michigan
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 ctggccaaggggttctacaactacggcgccttcgtcgccgccgccaactcgttctcgggc 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 GCAGAGCAATGTGGAAGCCAAGCTGGGGGTGCAGTGTGTCTCCGTTGGGCTCTGCTGCAGC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           418 actteceaegagaegaeeggeggtggeegaeggegeeegaeggeeetaeteetgggge 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 AAATTTGGGTGGTGTGGGAGCACAAACGAGTACTGTGGTGATGGCTGCCAAAGCCAATGT
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Pred. No. 3e-62; .
0; Mismatches 290; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA needed for chitinase OTHER INFORMATION: in elm.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         268 GGCGGCAGCGGTAGCGAT-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: chitinase encoding DNA
NAME: IAN C. MCLEOd
REGISTRATION NUMBER: 20,931
REFERENCE/DOCKET NUMBER: MSU 4.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (517) 347-4103
TELER: No. 5539056
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Ulmus Americana
STRAIN: NPS 3-487
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Best Local Similarity 64.0%;
Matches 575; Conservative
                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
HYPOTHETICAL: No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMMEDIATE SOURCE: N
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: N/P
CELL TYPE: N/A
CELL LINE: N/A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N/A
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                                                                                                                                                                                                                                                                                               goggogggagggtgoctgggtacggtgtgatcaccaacatcatcaacggtgggctcgag 837
                                                                                                                                                                                                                                                                                                               835 TCGGCCGGCCGAGTTCCGGGCTACGGCGTGATCACCAACATTATCAACGGTGGGATAGAA 894
                                                                                                                                                                                                                                                                                                                                                              tgogggcgcgggcaggacggccgtgtcgccggaccggatcgggttctacaagcgctactgc 897
                                                                                                                                                                                               GCAACTGACCCTGTCATTTCCTTCAAAACGGCCTTATGGTTCTGGATGACCCCACAGTCA 774
                                                                                                                                                                                                                                                                                                                                                                                             895 TGCGGGAAAGGTCAGGTTCCTCAGGTGGATCGGATTGGATTCTACAAGAGGTACTGT 954
535 TACTGCTACAATAGGGAGCAAAACCCTTCCTTCCGATTATTGTTCTTTTAGTCCTACTTGG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                               gacetecttggcgtcagetacggtgacaacetggactgetacaaaccaaaggeegtteg 955
                                ccatgtgcgccgggcaagaagtacttcgggcgcgggcccatccagatctcacaactac
                                                                                                                                                                gogtoggacgcgaccgtgtcgtttaagacggcgttgtggttctggatgacgccgcaatca
                                                                                                                                                                                                                              cccaagcettcgagccacgacgtgatcacgggccggtggagccetcgggcgccgaccag
                                                       CCTIGICITCCGGAAAGAGATACTTTGGCCGTGGTCCCATTCAACTCTCCTGGAACTAC
                                                                                                  aactacgggccggggggggggccatcggcaccgacctgctcaacaacccggaccttgtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Mascmeh B. Sticklen and Ravindra K. Hajela TITLE OF INVENTION: A Chitinase cDNA Clone From a TITLE OF INVENTION: Disease Resistant American TITLE OF INVENTION: Elm Tree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage COMPUTER: Acer
COMPUTER: Acer
MEDIUM SYSTEM: MS-DOS 5.00
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/603,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
COUNTRY: Okemos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-603-919-1; Sequence 1, Application US/08603919; Patent No. 5728382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (517) 347-4100
(517) 347-4103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 1225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: NO. 5728382e
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: Nucleic Acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Ian C. McLeod
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Masome
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58 geogageaatgeggetegeaggeeggegggegaegtgeeceaaetgeetetgetgeage 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 ctggccaaggggttctacaactacggcgccttcgtcgccgccaactcgttctcgggc 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGCCAAGGGGTTTTACACCTATGATGCTTTTTATTGCGGCTGCCAAGGCTTTCCCTGCA 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 ttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcgttcctcgctcag 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 actteceacgagacgaccgcgggggggccgacggcccgacggccctactcctggggc 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 ACTTCCCATGAAACTACAGGTGGGTGGGCAAGTGCACCCGACGGTCCATACTCTTGGGGA 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tactgottcaaccaggagcgcgcgccacctccgactactgcacgccgagctcgcagtgg 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                535 TACTGCTACAATAGGGAGCAAAACCCTTCTTCCGATTATTGTTCTTTTAGTCCTACTTGG 594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACTATGGACAGTGTGGAAGGGCCATAGGAGCAAACCTATTAAACAACCCTGATCTCGTA 714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 GCAGAGCAATGTGGAAGCCAAGCTGGGGGTGCAGTGTGTCCCGTTGGGCTCTGCTGCAGC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208 AAATTTGGGTGTGTGGGAGCACAAACGAGTACTGTGGTGATGGCTGCCAAAGCCAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 aatggetgeageggegeeceeggtaeeggtaeegaeeeeeteeggeggeggegtetee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      268 GGCGCAGCGGTAGCGAT----GACATTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238 tecattatetegeagtegetettegaceagatgetgetgeacegeaaegaegegtge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       295 GGTCTCATATCAAGCTCCGCCTTTAATGACATGCTTAAGCATCGTAACGACGGTGGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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Pred. No. 3e-62;
0; Mismatches 290; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: sequencing OTHER INFORMATION: DNA needed for chitinase OTHER INFORMATION: in elm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: chitinase encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           37.3%;
64.0%;
                                                                                                                                                           Ulmus Americana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 575; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             N/A :
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US-08-603-919-1
                                                                                                                                                                              STRAIN: NPS 3-487
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE: N
POSITION IN GENOME:
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Best Local Similarity
                                                                                                                                                                                                                                                                 N/A
                                                                                                                                                                                                                                                                                                                N/A
                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                           HAPLOTYPE: N/
TISSUE TYPE:
CELL TYPE: N/
CELL LINE: N/
TOPOLOGY: Lir
MOLECULE TYPE:
                                                                             S.
                                                 HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
                                                                                                                                                        ORGANISM:
                                                                                ANTI-SENSE:
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Gaps

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                                                                         cgtgtetgegeaegeegageaatgegetegeaggeeggeggggggaegtgeeeaaetg 104
                                                                                                                                                                                      72 TCTCTGCTGCTGCAAATTTGGTTGGTGTGGTAACACCCAATGACTATTGTGGCCCTGGCAA 131
                                                                                                                                                     cetetgetgeageaagtteggtttetgeggeaceacetecgaetaetgeggeacegge--
                                                                                                                                                                                                                             -tgccagagccagtgcaatggctgcagcggcggcacccggtaccggtaccgacccctc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291 TAGGTCTTTCCTGGCTTTGGTACTAGTGGTGATACCACTGCCCGTAAAAGAGAAATCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gatgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 GATGACTCCTCAATCACCAAAACCTTCTTGCCACGATGTCATCATTGGAAGATGGCAACC
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                                                                                                                                                                                                                                                                                                                       caacgacgcggcgtgcctggccaaggggttctacaactacggcgccttcgtcgccgccgc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             642 caacccggaccttgtggggtcggacgcgaccgtgtcgtttaagacggcgttgtggttctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ctcgggcgccgaccaggcggcggggggggggtgcctgggtacggtgtgatcaccaacatcat
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                                                                                                                                                                                                                                                                                                     cggcggcggcgtctcccattatctcgcagtcgctcttcgaccagatgctgctgcaccg
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                                      24;
 Length 943;
                                      Indels
Score 349.2; DB 2;
Pred. No. 1.6e-60;
); Mismatches 313;
                                                                                                                                                                                                                                                            132 TIGCCAGAGCCAGIGCCCIGGIGGICCCA----
                                      0;
 36.4%;
63.3%;
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                                      Conservative
                   Similarity
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US-07-842-165-15
                                    581;
   Query Match
                                                                                                                                                                                                                                                                                                     222
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                                   Matches
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APPLICANT: DEGNAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: TOPPAN, Alain
TITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
                                      111
                                                                         834
                                                                                                                837
                                                                                                                                    GCAACTGACCCTGTCATTTCCTTCAAAACGGCCTTATGGTTCTGGATGACCCCACAGTCA 774
                                                                                                                                                                                      tgegggegegggeaggaeggeegtgtegeegaeeggateggggttetaeaagegetaetge 897
                                                                                                                                                                                                            955 GATATCCTTAGAGTTGGCTATGGGAACAATCTTGATTGCTATAACCAGAGGCCTTTTG 1012
                                                                                                                                                                                                                                                              898 gacctccttggcgtcagctacggtgacaacctggactgctacaaccaaaggccgttcg 955
                                                                                                          778 goggoggggagggtgcctgggtacggtgtgtcaccaacatcatcacggtgggctcgag
                                                          CCAAAGCCCTCGTGCCATGACGTCATCACCGGAAGATGGAGTCCTTCCGGCACCGACCAG
                                      cocaagocttcgagccacgacgtgatcacgggccggtggagcccctcgggcgccgaccag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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3R: 16781/564/BEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Foley & Lardner: 3000 K Street, N.W., Suite 500 Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO PCT/FR91/00607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/475,427 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 21-JUL-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 09460
FILING DATE: 24-JUL-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 15, Application US/08475427
Patent No. 5859340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 1f TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
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(202)672-5399
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nucleic acid
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TOPOLOGY: lin
MOLECULE TYPE:
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; Sequence 15, Application US/07842165 ; Patent No. 5932698

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APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 17
  351 GGCTTTCTTCGCCCAAACCTCCCATGAACTACAGGAGGATGGGCAACAGCACCAGATGG 410
                                                                                                                                                        411 TCCATACGCGTGGGGTTACTGCTTGGCTTAGAGAACAAGGTAGCCCCGGCGACTACTGTAC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   582 gateteacacaactacaactacgggccggggggggggggcatcggcaccgacctgctcaa 641
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                                                                                                                                                                                                                                    gatgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagccc
                                                            cecetaetectggggetaetgetteaaceaggagegegegeeaeeteegaetaetgeae
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PatentIn Release #1.0, Version #1.25
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Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
Sela-Buurlage, Marianne B.
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APPLICATION NUMBER: US/08/047,413
FILING DATE: 19-APR-1993
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STREET: 755 Page Mill Road
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MEDIUM TYPE: Floppy disk
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CITY: Palo Alto
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APPLICANT:
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                                APPLICANT: GRISON, Rene
APPLICANT: LEGGAY, Jean-Jacques
APPLICANT: PIGNARD, Annie
APPLICANT: PIGNARD, Alain
IITLE OF INVENTION: Recombinant gene coding for a protein
TITLE OF INVENTION: having endochitinase activity or for a precursor thereof.
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                                                                                                                                                                                                        STREET: King Street Station, Suite 500, 1800 Diagonal STREET: Road, PO Box 299
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/842.165
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Pred. No. 1.6e-60;
0; Mismatches 313;
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                                                                                                                                                                                                                                                                                                                                                                                PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: SAXE, Bernhard D
REGISTRATION NUMBER: 28,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 16
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
                                                                                                                                                                                      ADDRESSEE: FOLEY & LARDNER
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63.38;
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(703) 683-4109
                  Michel
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INFORMATION FOR SEQ ID NO: SEQUENCE CRARACTER.ESTICS: LENGTH: 943 base pairs TYPE: NUCLEIC ACID
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Best Local Similarity 63.3'
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                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                            CITY: ALEXANDRIA STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
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SENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    USA
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APPLICANT: Bol, John F.
APPLICANT: Linthorst, Hubertus J.M.
TITLE OF INVENTION: FUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNUCLEOTIDES FOR USE THEREIN
882 TTACAGGAGGTATTGCAGTATTCTTGGTGTTAGTCCTGGTGACAATCTTGATTGCGGAAA
                                                               ctegggcgccgaccaggcgggggggggggggcctgggtacggtgtgatcaccaacatcat
                                                                                                                                                   caacggtgggctcgagtgcgggcgcgggcaggacggccgtgtcgccgaccggatcgggtt
                                                                                                                                                                                          822 CAATGGTGGCTTGGAATGTGGTGGTGGCACTGACTCAAGGGTCCAGGATCGCATTGGGTT
                                                                                                                                                                                                                                          ctacaagcgctactgcgacctccttggcgtcagctacggtgacaacctggactgctacaa
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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REGISTRATION NUMBER: 29,959
REGISCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cornelissen, Bernardus J.C.
Melchers, Leo S.
Meulanhoff, Elisabeth J.S.
van Roekel, Paroen S.C.
Sela-Buurlage, Marianne B.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/229,050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 10, Application US/08229050 Patent No. 6066491 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 1152 harr
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STATE: California
COUNTRY: USA
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TOPOLOGY: li
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US-08-229-050-10
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Pred. No. 3.3e-60;
0; Mismatches 314;
                                                                                                                                                 24615-20022.00
    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/647,831
FILING DATE: 29-7AN-1991
ATTORNEY/AGENI INFORMATION:
NAME: MUTASHIGO, Kate H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 24615-2002;
TELECHONE: 415-434-5600
TELEFAX: 415-494-0792
                                                                                                                                                                                                                                     TELEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 63.2%;
Matches 580; Conservative
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STRANDEDNESS: single
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CLASSIFICATION:
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US-08-047-413-10
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE:
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STATE: California
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US-08-801-563-10
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RESULT 13
US-08-801-563-10
                                                                             APPLICANT:
APPLICANT:
                                                     GENERAL INFOR APPLICANT:
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                                                                               24;
                                                     Length 1152;
                                                                               Indels
                                                  Score 347.6; DB 3;
Pred. No. 3.3e-60;
0; Mismatches 314;
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63.2%;
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APPLICANT: Lithtbort, Hubertus J.M.
TITLE OF INVENTION: PUNGAL RESISTANT PLANTS, PROCESS FOR
TITLE OF INVENTION: OBTAINING FUNGAL RESISTANT PLANTS AND RECOMBINANT
TITLE OF INVENTION: POLYNOCLEOTIDES FOR USE THERRIN
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 TCTCTGCTGCAGCAAATTTGGTTGGTGGTAACACCAATGACTATTGTGGCCCTGGCAA 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 3;
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Pred. No. 3.3e-60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-813-5600
TELEFAX. 41-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                  Cornelissen, Bernardus J.C
                                                                                     Melchers, Leo S.
Meulenhoff, Elisabeth J.S.
van Roekel, Jeroen S.C.
                                                                                                                                                      Sela-Buurlage, Marianne B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MBER: US 07/647,831
29-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/047,413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                             Vloemans, Alexandra A. Woloshuk, Charles P.
; Sequence 10, Application US/08801563; Patent No. 6087560; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                               Morrison & Foerster
755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/C
FILING DATE: 19-APR-1993
APPLICATION NUMBER: US 07/E
FILING DATE: 29-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MUNCAShige, Kate H.
REGISSTRATION NUMBER: 29,955
REFERENCE/DOCKET NUMBER: 29
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 1152 base pairs
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63.2%;
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                                                     MEDIUM TYEE: KIOPPY GIRK
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
GURRHY APPLICATION DATA:
APPLICATION NUMBER: US/08/475,427
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/842,165
FILING DATE: 01-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR91/00607
FILING DATE: 21-JUL-1991
PRIOR APPLICATION NUMBER: PR 90 09460
FILING DATE: 24-JUL-1990
ATTORNEY/AGBNT IMPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 289.6; DB 2;
Pred. No. 7.4e-49;
0; Mismatches 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 16781/564/BEDL. TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 905 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE: DNA (genomic)
US-08-475-427-14
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60.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (202)672-5300
                                           Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202)672-5399
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Matches 516; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                     COMPUTER READABLE FORM:
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TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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-- CACCACCCGG 221
                                              281
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                                                                                                                                                                                                                                                                                                                                                                 GGCTTTCTTCGCCCAAACCTCCCATGAAACTACAGGAGGATGGGCAACAGCACCAGATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           462 TCCATACGCGTGGGGGTTACTGCTGGCTTAGAGAACAATGTAGCCCCCGGCGACTACTGTAC
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                                              cggcggcggcgtctcctccattatctcgcagtcgctcttcgaccagatgctgctgcaccg
                                                                                       22 TGGTGGGGATCTCGGCAGTATCATCTCAAGTTCCATGTTTGATCAGATGCTTAAGCATG
                                                                                                                                       caacgacgcggcgtgcctggccaaggggttctacaactacggcgccttcgtcgccgccgc
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Patent No. 5859340
GENERAL INFORMATION:
APPLICANT: DUBOIS, Michel
APPLICANT: LEGUAY, Jean-Jacques
APPLICANT: PIGNARP, Annie
APPLICANT: PIGNARP, Annie
APPLICANT: POPPAN, Alain
183 TIGCCAGAGCCAGIGCCCIGGIGGICCCA
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CIIY: Washington, D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-475-427-14
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7

466 getegeagtggecatgtgegeegggeaagaagtaettegggegeggggeceateeagatet 586 Gaps 12;

us-09-534-229c-8.rni

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                                                                                        CIGCCTTGGCACAGAATTGTGGTTCACAGGCGGAGGCAAAGTTTGTGCGTCGGGACAAT 121
                                                                                                                                                                                                              233 ACCTCGGAAGCGTCATCTAAATTCTATGTTTGATCAAATGCTTAAGCATCGTAACGAAA 292
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                                                                                                                                                                                                                                                                            gocagitgcaaiggctgcagcggcggcaccccggitaccggitaccgacccccticcggcggcg
                                                                                                                                                                                                                                                                                                                       182 AAAGTCAGTGTCCAGGTGGCGGCCCTGGTCCTGGTCCTGT-----TACTGGTGGGG
                                             12;
  Length
                                             Indels
                                           324;
DB 2;
Score 289.6; DB 2
Pred. No. 7.4e-49;
0; Mismatches 324
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HVSME1002 HVSMEh009 WHE0982_G HVSME1000

PI1_65_E1 Zm06_01a0 HVSME1000 HVSMEh009

BG415203 B BG46884 BBG46884 BBG46884 BBG560345 W BE500345 W BE5003112 W BE500112 W BE500112 W BE500112 W BE500112 W BE500112 W BE600112 W BE600112 W BE600112 W BE454845 BBC4616 BBC4616 BBC4616 BBC60244 F BE600244 F BE600244 BBC60244 BBC6

AL500402 HVSMEh009

Searched:

Database

Result Š.

Sequence:

Run on:

HVSME1000 HVSME1000 HVSMEh009

WHE2054_D HVSMEh008

HVSME1002

WHE0978_E

Zm06_09b0 Zm06_02b0 P11_65_E1 Zm06_01a1 707094C01 Zm06_05f0 HVSMEi000 HVSMEh008

Zm06 06e0 HVSME1001 HVSMED001 HVSMEh01

BG368322 BG301220

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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                        Trificeae, Hordeum.
1 (Pariticeae, Hordeum.)
1 (Abses 1 to 705)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Wing, R., Close, T.J., Henry, D., Kernodle, S., Palmer, M., Rambo, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Y., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                                             BG367460 705 bp mRNA EST 08-MAR-2001
HVSME10012F13f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSME10012F13f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Development of a genetically and physically anchored EST resource for barley genomics
Unpublished (2000)
Contact: Wing RM
Clemson University Genomics Institute
Clemson University
100 Jordan Hall. Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. 705
//organism="Hordeum vulgare"
/dulityar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 690.
                                                                                  BG369588
BG365157
BG365326
BE454845
                                                                                                                     BE598085
BG836340
BG366294
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BG836379
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BE195290
BE405578
                       BE500345
BG366386
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BG301220
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                                                                   BG313150
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Hordeum vulgare
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350.2
349.6
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345.6
3345.6
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416.2
415
399.4
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355.8
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385.6
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AUTHORS
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BG367460
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BF064981 HV_CED002
BE502672 HVSME1010
BG365834 HVSME1000
BG365634 HVSME1000
BG365634 HVSME1000
BG368852 HVSME1002
BG414551 HVSME8001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BG367616 HVSMEi001
BE705117 SC02_08b0
BG365536 HVSMEi000
BG365857 HVSMEi000
                                                                     (without alignments)
3353.307 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BG367460 HVSME1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                               1 atgagaggagttgttggtggt.....accaaaggccgttcgcatag
                                                            3, 2002, 16:24:10 ; Search time 3076.35 Seconds
                                                                                                                                                                           22703874
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                         11351937 seqs, 5372889281 residues
                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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BE705117
BG365536
BG365857
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BG416746
BG368852
BG414551
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BE602672
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                                            OM nucleic - nucleic search, using sw model
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em_gss_vrt:*
em_gss_other:*
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Maximum Match 100%
Listing fixst 45 su
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gb_est1:*
gb_est2:*
gb_htc:*
gb_gss:*
em_gss_fun:*
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em_gss_pro:*
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Match Length
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111:
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17:
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436.8
434.3
430.8
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                                                                                                !itle:
Perfect score:
                                                                                                                                 Scoring table:
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Poales; Poaceae; Pooideae
              Triticeae; Hordeum.

1 (bases 1 to 711)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu.
X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 260 c 224 g 109 t.
                                                                                                                   Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tteggtttetgeggeaceaecteegactactgeggeaeegggetgeeagageeagtgeaat 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 TTCGGCTTCTGCGGCTCCACCTCCGACTACTGCGCGCACCGGCTGCCAAAGCCAGTGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                               20 DAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 11;
                                                                                                                                for barley genomics
Unpublished (2000)
Conteact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tea: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
Spermatophyta; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 572.8; DB 1 Pred. No. 1.2e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Hordeum vulgare
HVcDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                              /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEi0012P08f"
                                                                                                                                                                                                                                                                                                           678.
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Location/Qualifiers
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94.5%;
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1 (base
Wing,R.
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                                REFERENCE
AUTHORS
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                                                                             /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/parley/ To order a clone spite_1/*ww.genome.clemson.edu/orders" 261 c 219 g ttp://www.genome.clemson.edu/orders"
                                                                                                                                                                                                                                                         ä
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HYSME10012P08f HOrdeum vulgare 20 DAP spike EST library HYCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HYSME10012P08f, MRNA sequence.
BG367616
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                              gagcaatgeggetegeaggeeggegggggggegtgeeeaetgeetetgetgeageaag 120
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                                                                                                                                                                                                                                                         Gaps
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                  EST library
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                DAP spike
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                                                                                                                                                                                                                     Score 578.4; DB 1
Pred. No. 1.1e-98;
0; Mismatches 31
                20
                /clone_lib="Hordeum vulgare
HYCDNA010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
/clone="HVSME10012F13f"
                                                                                                                                                                                                                      60.28;
94.78;
                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                       Similarity
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SOURCE
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ORGANISM
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AUTHORS
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COMMENT
                459
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//dev_stage="seedling three-leaf stage"
//note="Vector: Bluescript SK+/Xhol-EcoRI; Site_1: Eco RI;
//stage.st 20c, 12 hrs light/day. Library made with
Stratagene UNIZAP XR Kit/(not packaged). cDNA is directly
ligated into SK+/Xhol-EcoRI, then electroporated into
// 10pl0 cells (livitrogen). It is others
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                                                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Puma (winter rye)"
db_xref="taxon:4550"
/clone="sc02_08b02"
/clone_lib="Sc02_AAFC_ECORC_cold_stressed_winter_rye_seedl
                                                                                                                                                                                                                                                                                                                                                                                                                 Hattori
                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooid Triticeae; Secale.

( Chases 1 to 681)
Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Hatt, J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings Unpublished (2000)
                                                                                                                                                                                                                              BE705117 681 bp mRNA EST 12-SEP-2000 SC02_88002_A SC02_AAFC_ECORC_cold_stressed_winter_rye_seedlings Sco2ale cereale cDNA clone Sc02_08b02, mRNA sequence. BE705117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, KIA 0C6, Canada
Tel: (613) 759-1662
Pax: (613) 759-1701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cogcaacgacgcggcgtgcctggccaaggggttctacaactacggcgccttcgtcgccgc 338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgccaactcgttctcggggcttcgcgaccacaggtagcaccgacgtcaagaagcgcgaggt 398
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537 gecatgigegecgggeaagaagiaetiegggegegggeecaiceagaieteacaeaaeta
                                                                          3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Secale cereale"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="leaf, crown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    singhja@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                          BE705117.1 GI:10093382
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Matches 621; Conservative
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KEYWORDS
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Triticeae; Hordeum.

1 (bases 1 to 805)
Wing, R., Close, T. J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu. Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HVSWE10003B22f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSWE10003B22f, mRNA sequence. BG365536
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                                                                                                                                                                                                                         504 ceccectacreseeseracrecrecracracrasses
                                                 ctggatgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggag
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/organism="Gordeum vulgare"
/cultivar="Morex"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 778.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:4513"
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Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          caaccaaaggccgttcgcatag 960
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Unpublished (2000)
Contact: Wing RA
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Hordeum vulgare
Enkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnollophyta: Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
1 (bases 1 to 935)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 338 c 290 g 156 t
nvsmrluuu4[09f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSMEi0004I09f, mRNA sequence. BG365857
                                                                                                                                                                                                                                                       Development of a genetically and physically anchored EST resource
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Contact: Wing RA Clemson University Genomics Institute Clemson University
100 Jordan Hall, Clemson, SC 29634, USA 161: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seg primer: AAITAAACCTCACTAAAAGGG
High quality sequence stop: 626.
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Pred. No. 2e-81;
0; Mismatches 200;
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/cultivar="Morex"
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/clone="HySMB10004109f"
/clone="Hordeum vulgare 20
HYCDMS010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="Sola"
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al Similarity 76.5%;
687; Conservative
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                       /clone_lib="Hordeum vulgare
HVcDNA0010 (20 DAP)"
/tissue_type="20 DAP spike"
/lab_host="SOLR"
          /clone="HVSMEi0003B22f"
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HV_CBD0022E17f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Erysiphe infected & control) Hordeum vulgare cDNA clone
HV_CBD0022E17f, mRNA sequence.
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le, S., Palmer, M., Rambo
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             tactgetteaaccaggagegegegeeceecteegactactgeacgeegagetegegtgg
ttogogaccacaggtagcaccgacgtcaagaagcgcgaggtggccgcgttcctcgctcag
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100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/cultivar="CI16151 (Mla6)"
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Seq primer: AATHAACCCTAAAGGG
High quality sequence stop: 792.
Location/Qualifiers
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BF064981
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For
                                                                                                                           more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 291 c 282 g 121 t
                                                                                                            EcoR1; Site_2: Xhol;
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Pred. No. 1.9e-76;
0; Mismatches 166;
/db_xref="taxon:4513"
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Hordeum.
I (bases I to 937)
Wing R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG365887 937 bp mRNA EST 08-MAR-2001
HVSMEi0004K07f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
CO DAP) Hordeum vulgare cDNA clone HVSMEi0004K07f, mRNA sequence.
BG365887 GI:13254986
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Unpublished (2000)
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                             595
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CCITCGCCIGGGGCIACTGCTICAAGCAGGAACGCGCCGCCTCCTCCGACIACTGCACCC 355
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/lab_host="SolR"
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Seq primer: AATAACCCTCACTAAAGGG
High quality sequence stop: 888.
Location/Qualifiers
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Fax: 864 656 4293
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Hordeum vulgare
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Wood,T.
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more details on library preparation and sequence analysis
see http://www.genome.clemson.edu/projects/barley/ To
see http://www.genome.clemson.edu/orders"
10 thers
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Hordeum vulgare
Hordeum vulgare
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                       BE602672 729 bp mRNA EST 02-WAR-2001
HVSMEh0101A21f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0101A21f,
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 729)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y.
X., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo
,T., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and
Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Development of a genetically and physically anchored EST resource for barley genomics for barley genomics from the forbulished (2000) Contact: Wing RA Clemson University Genomics Institute
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Pred. No. 3.1e-76;
0; Mismatches 128; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/organism="Hordeum vulgare"
/cultivar="Morex"
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Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 713.
Location/Qualifiers
                                                                                                                                                                                             BE602672.1 GI:9860233
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80.98;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; ; Triticeae; Hordeum.
1 (bases 1 to 742)

REFERENCE AUTHORS

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3
see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 332 c 276 g 175 t
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                                                                                Score 453.6; DB 11; Length
Pred. No. 2.3e-75;
0; Mismatches 164; Indels
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77.5%;
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BG365634 742 bp mRNA EST 08-MAR-2001 HVSME10003102f Hordeum vulgare 20 DAP spike EST library HVcDNA0010 (20 DAP) Hordeum vulgare cDNA clone HVSME10003102f, mRNA sequence.

GI:13254733

BG365634.1 BG365534

DEFINITION

LOCUS

BG365634

ACCESSION

VERSION KEYWORDS

Hordeum vulgare

ORGANISM

SOURCE

barley.

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/tissue_type="20 DAP spike"
/lab_host="SOLR"
/lab_host="Yector: lambdaAAP, Site_1: EcoRl; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/Darley/ To order a clone see http://www.genome.clemson.edu/orders"
a 259 c 240 g 121 t lothers
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Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and Wood, T.
                                                                           Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
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Pred. No. 1.2e-72;
0; Mismatches 116;
                                                                                                                                          Contact: Wing RA
Clemson University Genomics Institute
Clemson University
In Underman Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="HVSMEi0003102f"
/clone_lib="Hordeum vulgare
HVcDNA0010 (20 DAP)"
                                                                                                                                                                                                                                                                                                                                                                           /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 707.
Location/Qualifiers
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/db_xref="taxon:4513"
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Best Local Similarity 81.4%;
Matches 508; Conservative
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Mariadiphyta; Mariadiphyta; Mariadiphyta; Mariadiphyta; Mariadiphyta; Diliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.

1 (bases 1 to 625)
Wing.R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Anderson,H., Dale,J., Henry,D., Kernodle,S., Palmer,M., Rambo,Y.., Saski,C., Schwartzbeck,J., Simmons,J., Choi,D.W., Main,D. and Wood,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG368854 625 bp mRNA EST 08-MAR-2001
HVSMEi0020P07f Hordeum vulgare 20 DAP spike EST library HVCDNA0010
(20 DAP) Hordeum vulgare cDNA clone HVSMEi0020P07f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000)
Contact: Wing RA
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  181 GCGCTACTACGCCCCCCCCCCCCCCCCCCCCCCCCCACACTACAACTATGGACCTGCCGG
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                                                                gogogogocacctccgactactgcacgccgagctcgcagtggccatgtgcgccgggcaa
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                                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics Institute
Clemson University
100 Tordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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/clone="EVSMEi0020p07f"
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seg primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 16
High quality sequence stop: 606.
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1 (bases 1 to 908)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                                                              BG415203 908 bp mRNA EST 13-MAR-2001
HVSMEk0005116f Hordeum vulgare testa/pericarp EST library
HVcDNA0013 (normal) Hordeum vulgare cDNA clone HVSMEk0005116f, mRNA
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Contact: Wing RA
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/cultivar="Morex"
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/clone="HVSMER0005116f"
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HVCDMA0013 (mmmal)"
/tissue_type="testa/pericarp"
/lab_host="#UC121"
                                                                                                                        cgggcgccgaccaggcggcggggggggggggcctgggtacggtgtgatcaccaacatcatca 823
                                                                                                                                               435 eggegggtggeegaeggegeeegaeggeeetaetteetggggetaetgetteaaeeagga 494
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ACCCGGACCTGGTGGCCACGGACGCCACTGTGGCGTTTAAGACGGCCATCTGGTTCTGGA
                                                                  TGACGGCGCAACCGCCCAAGCCGTCGAGCCATGCTGTGATCGCCGGCCAGTGGACCCCGT
                                          tgacgccgcaatcacccaagccttcgagccacgacgtgatcacgggccggtggagcccct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 423.4; DB 11; Length 9
Pred. No. 1e-69;
0; Mismatches 101; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAGGG
High quality sequence stop: 1815.
Location/Qualifiers
                                                                                                                                                                                                                             acggtgggctcgagtgcgggcgcgggcagg 853
                                                                                                                                                                                                                                                                                                                                                                                                                              BG415203
BG415203.1 GI:13320754
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Best Local Similarity 82.7%;
Matches 484; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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Wood,T.
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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547
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AUTHORS
                                      704
                                                                               607
                                                                                                                      764
                                                                                                                                                              667
                                                                                                                                                                                                     824
                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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BG415203
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194
                                                                      ,T., Sa
Wood,T.
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                               REFERENCE
                                         AUTHORS
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                                                                                                TITLE
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HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0093N17f,
                                                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To see http://www.genome.clemson.edu/orders" 223 c 202 g 93 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          barley.
Hordeum vulgare
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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                                                                                                                                                                                                                       235 tectecattatetegeagtegetettegaceagatgetgetgeacegeaacgaegeggeg 294
                                                                                                                                                                                                                                                                              354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 CGGGCAGCGGGCCGGGTGCCCGGGTTTGGGCGTGATCACCAACATCGTCAACGGCGGGGAT 601
                                                                                                                                                                                                                                                                                                                                                            GGCTTCGGCACCACCGGCGGAACCGACACCGGAAGCGCGAGGTGGCCGCCTTCCTGGCC 181
                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                             295 tgcctggccaaggggttctacaactacggcgccttcgtcgccgccaactcgttctcg
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H
                                                                                                                                                                     Length 625;
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                                                                                                                                                                  Score 420.6; DB 11;
Pred. No. 3.2e-69;
); Mismatches 120; I
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BE454366
BE454366.2 GI:13189266
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80.6%;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
                                                                                      Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 312 c 280 g 181 t 2 others
                                                                                                                                                                                                       Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HycNn4009 (5 to 45 DAP)"
//tissue_nepe="5-45 DAP Spike"
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                                                                                                                                                                                                                   for barners of a yencarcarry and puysicarry ancient 551 for barners (2000)
On Jul 26, 2000 this sequence version replaced gi:9462873.
Contact: Wing RA
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7228
Fax: 864 656 4293
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Pred. No. 2.2e-68;
0; Mismatches 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 616.
Location/Qualifiers
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/db_xref="taxon:4513"
/clone="HVSMEh0093N17f"
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Best Local Similarity 77.0%;
Matches 535; Conservative
                                      ; Triticeae; Hordeum
I (bases 1 to 969)
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Search completed: May 3, 2002, 16:24:30 Job time: 7230 sec